

FIGURE 1

CCAGGTCCAAC TGCACCTCGGTTCTATCGATTGAATTCCCGGGGATCCTCTAGAGATCCCT
CGACCTCGACCCACGCGTCCGCCAAGCTGGCCCTGCACGGCTGCAAGGAGGCTCCTGTGGA
CAGGCCAGGCAGGTGGGCTCAGGAGGTGCCTCCAGGCGGCCAGTGGGCTGAGGCCCCAGC
AAGGGCTAGGGTCCATCTCCAGTCCAGGACACAGCAGCGGCCACCATGGCCACGCTGGGC
TCCAGCAGCATCAGCAGCCCCAGGACCGGGGAGGCACAGGTGGCCCCCACCACCCGAGG
AGCAGCTCCTGCCCTGTCCGGGGGATGACTGATTCTCTCCGCCAGGCCACCCAGAGGAGA
AGGCCACCCCGCTGGAGGCACAGGCCATGAGGGGCTCTCAGGAGGTGCTGCTGATGTGGCT
TCTGGTGTGGCAGTGGGCGGCACAGAGCACGCTACCGGCCCGCCGTTAGGGTGTGTGCT
GTCCCGGGCTCACGGGACCTGTCTCCGAGTCGTTCTGTCAGCGTGTGTACCAGCCCTTCC
TCACCACCTGCGACGGGCACCGGCCCTGCAGCACCTACCGAACCATTTATAGGACCGCTAC
CGCCGAGCCCTGGGCTGGCCCTGCCAGGCTCGCTACGCGTGTGCCCCGGCTGGAAGAG
GACCAGCGGGCTTCTGGGGCTGTGGAGCAGCAATATGCCAGCCGCATGCCGGAACGGAG
GGAGCTGTGTCCAGCCTGGCCGCTGCCCTGCAGGATGGCGGGGTGACACTTGCCAG
TCAGATGTGGATGAATGCAGTGTCTAGGAGGGGCGGCTGTCCCCAGCGCTGCATCAACACCGC
CGGCAGTTACTGGTGCCAGTGTGGGAGGGGCACAGCCTGTCTGCAGACGGTACACTCTGTG
TGCCCAAGGGAGGGCCCCCAGGGTGGCCCCAACCCGACAGGAGTGGAAGTGAATGAAG
GAAGAAGTGCAGAGGCTGCAGTCCAGGTGGACCTGCTGGAGGAGAAGCTGCAGCTGGTGTCT
GGCCCCACTGCACAGCCTGGCCTCGCAGGCACTGGAGCATGGGCTCCCGGACCCCGGCAGCC
TCCTGGTGCCTCTTCCAGCAGCTCGGCCGCATCGACTCCCTGAGCGAGCAGATTTCCTTC
CTGGAGGAGCAGCTGGGGTCTGCTCTGCAAGAAAGACTCGTGACTGCCAGCGCCCCAGG
CTGGACTGAGCCCTCACGCGGCCCTGCAGCCCCATGCCCTGCCCAACATGCTGGGGGTG
CAGAAGCCACCTCGGGGTGACTGAGCGGAAGGCCAGGCAGGGCCTTCTCTTTTCTCTCTC
CCCTTCCCTCGGGAGGGTCCCCAGACCCTGGCATGGGATGGGCTGGGATTTTTTTTGTGAAT
CCACCCCTGGCTACCCCCACCCTGGTTACCCCAACGGCATCCCAAGGCCAGGTGGGCCCTCA
GCTGAGGGAAGGTACGAGTTCCTCTGCTGGAGCCTGGGACCATGGCACAGGCCAGGCAGCC
CGGAGGCTGGGTGGGGCTCAGTGGGGGCTGCTGCCTGACCCCGACACAATAAAATGAAA
CGTGAAAAA
AGAGTCGACCTGCAGAAGCTTGGCCGCATGGCCCAACTTGTTTATGTCAGCTTATAATGGT
TACAAAT

FIGURE 2

MTDSFPPPGHPEEKATPPGGTGHEGLSGGAADVASGVSGRHRARLPARPLGCVLSRAHGDFV
SESFVQRVYQPFLLTTCDGHRACSTYRTIYRTAYRRSPGLAFARPRYACCPGWKRTSGLPGAC
GAAICQPPCRNGGSCVQPGRCRCFAGWRGDTQCSDVDECSARRGGCPQRCINTAGSYWCQCW
EGHSLSADGTL CVPKGGPPRVAPNPTGVDSAMKEEVQRLQSRVDLLEEKQLQLVLAPlHSLAS
QALEHGLPDPGSLLVHSFQQLGRI DLSLEQISFLEEQLGSCSCKKDS

Signal sequence:

amino acids 1-19

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 93-97, 270-274

N-myristoylation sites.

amino acids 19-25, 78-84, 97-103, 100-106, 103-109, 157-163,
191-197, 265-271

Amidation site.

amino acids 26-30

Aspartic acid and asparagine hydroxylation site.

amino acids 152-164

Cell attachment sequence.

amino acids 130-133

EGF-like domain cysteine pattern signature.

amino acids 123-135

FIGURE 3

CGCTCGCCCGCTCGCCCTCGCCTCCCCGAGAGTCCCTCGCGGCAGAGATGTGTGTGGG
GTCAGCCCACGGCGGGGACTATGGTGAAAATCCCGGCGCTCAGCAGTACTGCGCCCTGATC
CGGTCTCTTGGTGCCCTGGGCATCACCAACATAGCCATCGACTTCGGGGAGCAGGCCCTTGAA
CCGGGGCATTGCTGCTGTCAAGGAGGATGCAGTCAGATGCTGGCCAGCTACGGGCTGGCGT
ACTCCCTCATGAAGTTCCTTACGGGTCCCATGAGTGACTTCAAAAATGTGGGCTGGTGT
GTGAACAGCAAGAGAGACAGGACCAAAGCCGTCTGTGTATGGTGGTGGCAGGGGCCATCGC
TGCCGTCTTTACACACTGTATAGCTTATAGTGATTTAGGATACACTATATCAATAAACTGC
ACCATGTGACAGAGTCGGTGGGGAGCAAGACGAGAAGGGCCTTCTGTACCTCGCCGCTTT
CCTTTCATGGACGCAATGGCATGGACCATGCTGGCATTCTCTTAAAAACAATAACAGTTT
CCTGGTGGGATGTGCCTCAATCTCAGATGTATAGCTCAGGTGTGTTTTGTAGCCATTTTGC
TTCACAGTCACCTGGAATGCCGGGAGCCCTGCTCATCCCGATCCTCTCCTTGTACATGGGC
GCACCTGTGCGCTGCACCACCCTGTGCCTGGGCTACTACAAGAACATTACGACATCATCCC
TGACAGAAGTGGCCCGGAGCTGGGGGGAGATGCAACAATAAGAAAGATGCTGAGCTTCTGGT
GGCCTTTGGCTCTAATTCTGGCCACACAGAGAATCAGTCGGCCTATTGTCAACCTTTCTGTT
TCCCGGGACCTTGGTGGCAGTTCTGCAGCCACAGAGGCAGTGGCGATTGTTGTAGCCATTTGAC
CCCTGTGGGTACATGCCATACGGCTGGTTGACGGAAATCCGTGCTGTGTATCCTGCTTTCG
ACAAGAATAAACCCGAGCAACAACCTGGTGAGCACGAGCAACAGTTCAGCGCAGCCCACTC
AAGAAGTTCACCTTCTGCTGCATGGCTCTGTCACTCAGCCTGTTTCTGTGATGTTTGGAG
ACCCAACGTGTCTGAGAAAATCTTGATAGACATCATCGGAGTGGAATTTGCCTTTGACAGAAC
TCTGTGTTGTTCTCTTTCGCGATCTTCTCCTTCTTCCAGTTCAGTCAGAGTGGGCGCAT
CTCACCGGTGGCTGATGACACTGAAGAAACCTTCGTCCTTGCCCCAGCTCTGTGCTGCG
GATCATCGTCTCATCGCCAGCCTCGTGGTCTACCTTACTTGGGGGTGCACGGTGCAGCCC
TGGCGTGGGCTCCCTTCTGGCGGGCTTTGTGGGAGAATCCACCATGCTCGCCATCGCTGCG
TGCTATGCTACCGGAAGCAGAAAAGAAGATGGAGAATGAGTCGGCCACGGAGGGGGAAGA
CTCTGCCATGACAGACATGCCTCCGACAGAGGAGTGACAGACATCGTGGAAATGAGAGAGG
AGAATGAATTAAGGCACGGGACGCCATGGGCACTGCAGGGACCGTTCAGTCAGGATGACACTTC
GGCATCATCTCTTCCCTCTCCCATCGTATTTTGTTCCTTTTGTGTTTTGTTTGGTAAAT
GAAAGAGGCCTTGATTTAAAGGTTTCGTGTCAATTCCTAGCATCTGGGTATGCTCACACT
GACGGGGGACCTAGTGAATGGTCTTTACTGTGCTATGTAAAAACAAACGAAACAACTGAC
TTCATACCCCTGCCTCAGGAAACCCAAAAGACACAGCTGCCTCAGCGTTGACGTTGTGTCC
TCTCCCTGGACAATCTCCTCTTGGAACCAAGGACTGCAGCTGTGCCATCGCGCTCGGT
CACCTTGACAGCAGGCCACAGACTCTCCTGTCCCTTTCATCGCTCTTAAGAATCAACAGG
TTAAAACTCGGCTCTCTTTGATTGCTTCCCACTACATGGCCGTACAAGAGATGGAGCCC
CGGTGGCTCTTAAATTTCCCTTCTGCCACGGAGTTCGAAACCATCTACTCCACATGCGAG
GAGCGGGTGGCAGCTGCAGCCCGAGTCCCGTTTCACTGAGGAACGGAGACCTGTGAC
CACAGCAGGCTGACAGATGGACAGAATCTCCGTAGAAAGGTTTGTGTTGAAATGCCCGGG
GGCAGCAAACTGACATGGTTGAATGATAGCATTTCACTCTGCGTTCTCTTAGATCTGAGCAA
GCTGTCACTTCTACCCCCACCGTGTATATACATGAGCTAACTTTTTAAATTTGTCAAAAA
GCGCATCTCCAGATTCCAGACCCTGCCGCATGACTTTCTGAAGGCTTGTCTTCCCTCGC
CTTTCTGAAGTTCGATTAGAGCGAGTCACATGGAGCATCTTAACTTTGATTTTGTAGTTT
TACAGCTGACTGAAGCTTTAAGTCTCATCCAGCATTTCTAATGCCAGTTTGTGTAGGTAAC
TTTTGAAGTAGATATATTACCTGGTCTGCTATCCTTAGTCATAACTCTCGCGGTACAGGTAA
TTGAGAATGTACTACGGTACTTCCCTCCCACACCATACGATAAAGCAAGACATTTTATAAGC
ATACAGAGTCACTATGTGGTCTCCCTGAAATAACGCATTTCGAATCCATGTCAGTCTGAGT
TATTTTTCTAAGTTTGTGAAGCAGGTTTTTCTCTTAAAAAAATTTATAGACACGGTTCAC
AAATGTATTTAGTCAGAATTCCTAGACTGAAAGAACCTAAACAAAAAATATTTTAAAGATA
TAAATATATGCTGTATATGTATGTAAATTTTAAAGGCTATAATACATTTCTTATTTTTCG
ATTTTCAATAAAATGTCTCTAATACAAAAA

FIGURE 4

MVKFPALTHYWPLIRFLVPLGITNIAIDFGEQALNRGIAAVKEDAVEMLASYGLAYSLMKFF
TGPMSEDFKNVGLVFVNSKRDRTKAVLCMVVAGAIAAVFHTLIAYSIDLGYIIINKLHHVDESV
GSKTERRAFLYLAAPFMDAMAWTHAGILLKHKYSFLVGCASISDVIAQVVFVAILLHSHLEC
REPLLIPILSLYMGALVRCTTLCCLGYKNIHDIIPDRSGPELGGDATIRKMLSFWWPLALIL
ATQRI SRPIVNL FVS RDLGGSSAATEAVAILTATYPVGHMPYGWLTEIRAVYPAFDKNNPSN
KLVSTSNVTAAHIKKFTFVCMALSLTLCFVMFWTPNVSEKILIDIIGVDFAPAEELCVVPLR
IFSFFPVPTVRAHLTGWMLTKKTFVLAPSSVLRIIVLIASLVVLPYLGVBHATLGVGSL
AGFVGESTMVAIAACYVRKQKKMENESATEGEDSAMTDMPTTEEVTDIVEMRENE

Transmembrane domains:

amino acids 86-106, 163-179, 191-205, 237-253, 327-343, 357-374,
408-423, 431-445

FIGURE 5

CCTGACAGAAGTGCCCCGGAGCTGGGGGAGATNCAACATTAAAGAAGATGCTGAGCTTCTGGT
GCCNTTTGGCTCTAATTCTGGCCACACAGAGAANCAGTCGGCCTATTGTCAACCTCTTTGTT
TCCCGGGACCTTGGTGGCAGTTCTGCAGCCACAGAGGCAGTGGCGATTTTGACAGCCACATA
CCCTGTGGGTCACATGCCATACGGCTGGTTGACGGAAATCCGTGCTGTGTATCCTGCTTTG
ACAAGAATAACCCAGCAACAACTGGTGAGCACGAGCAACACAGTCACGGCGGCCACATC
AAGAAAGTTCACCTTCGTCTGCATGGCTCTGTCACTCACGCTCTGTTTCGTGATGTTTTGGAC
ACCCAACGTGTCTGNGAAATCTTGATAGACATCATCGGAGTGGACTTTGCCTTTGCAGAAC
TCTGTGTTGTTCTTTTGGGATCTTCTCCTTCTCCAGTTCAGTCACAGTGAGGGCGCAT
CTCACCGGGTGGCTGATGACACTGAAGAAAACCTTCGTC

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FIGURE 6

TGACGGAATCCCGGGCTGGGTATCCTGGTTTNGACAAGATAAACCCCCAGCAANAAATTGGG
GAGCAGGGCAAAACAGTNACGGGCAGCCCACATCAAGAAGTTCACCTTNGTTTGNATGGNTC
TGTCAACTCACGCTNTGTTTCGTGATGTTTTGGACACCCAAAGTGTTTGAGAAAAATTTGAT
AGACATNATCGGAGTGGANTTTGCCTTTGCAGAANTTTGNGNTGTTCCCTTGC GGATTTTCT
CCTTTTTCCAGTTCAGTCACAGNGAGGGCGCATCTACCGGGNGGNTGATGACANTGAAG
AAAACCTTTGTCCTTGCCCCAGCTINTTTGGTGCGGATCATTGTCCTNATNGCCAGCCTTGT
GGTCCTACCCTACCTGGGGGTGCACGGTGCGACCCTGGGCGTGGGTTCCCTCCTGGCGGGCA

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FIGURE 7

TATTCCCAGTTCCGGTCACGGGGAGGGCGCATNTCACCGGGTGGCTGANGACACTGAAGAAA
ACCTTNGTCCTTGCCCCCAGNTTTGTGNTGCGGATNATCGTCCTCATCGCCAGCCTNGTGGT
CCTACCCTACCTGGGGGTGCACGGTGAGAC

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FIGURE 8

GCCCCGCGCCCGGCGCCGGGCGCCCGAAGCCGGGAGCCACCGCCATGGGGGCCTGCCTGGGA
GCCTGCTCCTTGCTCAGCTGCGCGTCTTGCTCTGCGGCTCTGCCCCTGCACTCTGTGCAG
CTGCTGCCCCCGCAGCCGCAACTCCACCGTGAGCCGCTCATCTTCACGTTCTTCTCTTCC
TGGGGGTGCTGGTGTCCATCATTATGCTGAGCCCGGGCGTGGAGAGTCAGCTCTACAAGCTG
CCCTGGGTGTGTGAGGAGGGGCGCGGATCCCCACCGTCTGCAAGGGCCACATCGACTGTGG
CTCCTGCTTGGCTACCGCGCTGTCTACCGCATGTGCTTCGCCACGGCGGCTTCTTCTTCT
TCTTTTTTACCCTGCTCATGCTCTGCGTGAGCAGCAGCCGGGACCCCCGGGCTGCCATCCAG
AATGGGTTTTTGGTTCTTTAAGTTCTTGATCCTGGTGGGCTCACCGTGGGTGCCTTCTACAT
CCCTGACGGCTCCTTACCAACATCTGGTTCTACTTCGGCGTCGTGGGCTCCTTCTCTTCA
TCCTCATCCAGCTGGTGTGCTCATCGACTTTGCGCACTCCTGGAAACAGCGGTGGCTGGGC
AAGGCCGAGGAGTGCGATTCCCGTGCCTGGTACGCAGGCCCTTCTTCTTCTCACTCTCCTCTT
CTACTTGCTGTGATCGCGGCGGTGGCGCTGATGTTTATGTACTACACTGAGCCAGCGGCT
GCCACGAGGGCAAGGTCTTATCAGCCTCAACCTCACCTTCTGTGTCTGCGTGTCCATCGCT
GCTGTCTGCCCAAGGTCCAGGACGCCCAGCCAACTCGGGTCTGCTGCAGGCCTCGGTGAT
CACCTCTACACCATGTTTGTACCTGGTCAGCCCTATCCAGTATCCCTGAACAGAAATGCA
ACCCCCAATTGCCAACCCAGCTGGGCAACGAGACAGTTGTGGCAGGCCCGAGGGCTATGAG
ACCCAGTGGTGGGATGCCCCGAGCATTTGTGGGCTCATCATCTTCTCTCTGTGCACCTCTT
CATCAGTCTGCGCTCCTCAGACCACCGGCAGGTGAACAGCCTGATGCAGACCAGGAGTGCC
CACCTATGTAGTACGCCACACAGCAGCAGCAGCAGGTGGCAGCCTGTGAGGGCCGGGCC
TTTGACAACGAGCAGGACGGCGTCACCTACAGCTACTCCTTCTTCCACTTCTGCTGGTGT
GGCCTCACTGCACGTATGATGACGCTCACCAACTGGTACAAGCCCGGTGAGACCCGAAGA
TGATCAGCACGTGGACCGCGGTGTGGGTGAAGATCTGTGCCAGCTGGGCAGGGCTGCTCCTC
TACCTGTGGACCTTGTAGCCCCACTCCTCCTGCGCAACCGCACTTCAGCTGAAGGCACCT
CACAGCCTGCCATCTGGTGCTCTGCCACCTGGTGCCTCTCGGCTCGGTGACAGCCAACCT
GCCCCCTCCCCACCAATCAGCCAGGCTGAGCCCCACCCCTGCCCCAGCTCCAGGACCTG
CCCCTGAGCCGGGCTTCTAGTCGTAGTGCTTCAGGGTCCGAGGAGCATCAGGCTCCTGCA
GAGCCCCATCCCCCGCCACCCACACGGTGGAGCTGCCTCTTCTTCCCTCTCTCCCTGT
TGCCCATACTCAGCATCTCGGATGAAAGGGCTCCCTTGTCTCAGGCTCCACGGGAGCGGG
CTGCTGGAGAGAGCGGGGAATCCACCACAGTGGGGCATCCGGCACTGAAGCCCTGGTGT
CCTGGTCACGTCCCCAGGGACCTGCCCCCTCTCTGGACTTCGTGCCTTACTGAGTCTCT
AAGACTTTTTCTAATAAACAAGCCAGTGCGTGTAAAAAAA

FIGURE 9

MGACLGACSLSCASCLCGSAPCILCSCCPASRNSTVSRLIPTFFFLFLGVLVSIIMLSPGVE
SQLYKLPWVCEEAGIPTVLQGHIDCGSLLGYRAVYRMCFATAAFFFFFFFFTLLMLCVSSSRD
PRAAIQNGFWFFKFLILVGLTVGAFYIPDGSFTNIWFYFGVVGSLFLFILIQLVLLIDFAHSW
NQRWLGKAEECDRAWYAGLFFFTLLFYLLSIAAVALMFMYYTEPSGCHEGKVFISLNLTFC
VCVSIAAVLPKVQDAQPNSGLLQASVITLYTMFVTWSALSSIPEQKCNPHLPTQLGNETVVA
GPEGYETQWWDAPSIVGLIIFLLCTLFISLRSSDHRQVNSLMQTEECPPMLDATQQQQQVA
ACEGRAFDNEQDGVITYSYFFHFCLVLASLHVMMTLTNWYKPGETRKMISTWTAVVWKICAS
WAGLLLYLWTLVAPLLLRNRDFS

Signal sequence:

amino acids 1-20

Transmembrane domains:

amino acids 40-58, 101-116, 134-150, 162-178, 206-223, 240-257,
272-283, 324-340, 391-406, 428-444

FIGURE 10

GAGCGAGGCCGGGACTGAAGGTGTGGGTGTGAGCCCTCTGCGAGAGGGTTAACCTGGGTC
AAATGTCACGGATTCTCACCTCGTACAGTTACGCTCTCCCGCGGCACGTCGCGAGGACTTGA
AGTCTCGAGCGCTCAAGTTTGTCCGTAGGTGAGAGAGAAGGCCATGGAGGTGCCGCCACCGGC
ACCGCGGAGCTTTCTCTGTAGAGCATTGTGCCATTATTTCCCGAGTCTTTGTGTCGCGAAGCTG
TGACTGCCGATTTCGGAAGTCTTTGAGGAGCGTCAGAAGCGGCTTCCCTACGTCCTCAGAGCCC
TATTACCCGGAATCTGGATGGGACCGCTCCGGGAGCTGTTTGCCAAAGATGAACAGCAGAG
AATTTCAAAGGACCTTGCTAATATCTGTAAGACGGCAGCTACAGCAGGCATCATTGGCTGGG
TGTATGGGGGAATACCAGCTTTTATTCATGCTAAACAACAATACATTGAGCAGAGCCAGGCA
GAAATTTATCATAACCGGTTTGATGCTGTGCAATCTGCACATCGTGCTGCCACACGAGGCTT
CATTCTGTTATGGCTGGCGCTGGGGTTGGAGAACTGCAGTGTGTTGTGACTATATTCAACACAG
TGAACACTAGTCTGAATGTATACCGAAATAAAGATGCCCTTAAGCCATTTTGTAATTGCAGGA
GCTGTACGGGAAGTCTTTTAGGATAAACGTAGGCCTGCGTGGCCTGGTGGCTGGTGGCAT
AATTGGAGCCTTGCTGGGCACTCCTGTAGGAGGCCTGTGATGGCATTTCAGAAGTACGCTG
GTGAGACTGTTTCAGGAAAGAAAACAGAAGGATCGAAAGGCACTCCATGAGCTAAAACTGGAA
GAGTGGAAAGGCAGACTACAAGTTACTGAGCACCTCCCTGAGAAAATTGAAAGTAGTTTACG
GGAAGATGAACCTGAGAATGATGCTAAGAAAATTGAAGCACTGCTAAACCTTCCTAGAAACC
CTTCAGTAATAGATAAAACAAGACAAGGACTTGAAAGTGCTCTGAACTTGAACTCACTGGAGA
GCTGAAGGGGAGCTGCCATGTCCGATGAATGCCAACAGACAGGCCACTCTTTGGTCAGCCTGC
TGACAAATTTAAGTGCTGGTACCTGTGGTGGCAGTGGCTTGCTCTTGCTTTTTCTTTTCTT
TTTAACTAAGAATGGGGCTGTTGTA

FIGURE 11

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA23318

><subunit 1 of 1, 285 aa, 1 stop

><MW: 32190, pI: 9.03, NX(S/T): 2

MEVPPPAPRSFLCRALCLFPRVFAAEAVTADSEVLEERQKRLPYVPEPYYPESGWDRLRELF
GKDEQQRISKDLANICKTAATAGIIGWVYGGIPAFIHAKQQYIEQSQAIEYHNRFDAVQSAH
RAATRGFIRYGWRWGWRTAVFVTIFNTVNTSLNVYRNKDALSHFVIAGAVTGS�FRINVGLR
GLVAGGIIGALLGTPVGGLLMAFQKYAGETVQERKQKDRKALHELKLEEWKGRQLQVTEHLPE
KIESSLREDEPENDAKKIEALLNLPRNPVIDKQDKD

Important Features:

Signal Peptide:

amino acids 1-24

Transmembrane domains:

amino acids 76-96 and 171-195

N-glycosylation site:

amino acids 153-156

FIGURE 12

CGGAAGTCCCTTGAGGAGCGTCAGAAGCGGCTTCCCTACGTCCCAGAGCCCTATTACCCGGA
ATCTGGATGGGACCGCTCCGGGAGCTGTTTGGCAAAGATGAACAGCAGAGAAATTTCAAAGGA
CCTTGCTAATATCTGTAAGACGGCAGCTACAGCAGGCATCATTTGGCTGGGTGTATGGGGGAA
TACCAGCTTTTATTCATGCTAAACAACAATACATTGAGCAGAGCCAGGCAGAAATTTATCAT
AACCGGTTTGATGCTGTGCAATCTGCACATCGTGTGCCACACGAGGCTTCATTTCGTTTCATG
GCTGGCGCCGAACC

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FIGURE 13

TCAAGTTTGTCCGTAGGTCGAGAGAAGGCCATGGAGGTGCCGCCACCGGCACCGCGGAGCTT
TTTTCTGTAGAGCATTGTGCTTATTTCCCGAGTTTTTGTGCTGCCGAAGCTGTGACTGCCGAT
TCGGAAGTCCTTGAGGAGCGTCAGAAGCGGCTTCCCTACGTCCCAGAGCCCTATTACCCGGA
ATTTGGATGGGACCGCCTCCGGGAGCTGTTTGGCAAAGATGAACAGCAGAGAATTTCAAAGG
ACCTTGCTGATATNTGTAAGACGGCAGCTACAGCAGGCATCATTGGCTGGGTGTATGGGGGA
ATACCAGCTTTTATTCATGNTAAACAACAATACATTGAGCAGAGCCAGGCAGAAATTTATNA
TAACC

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FIGURE 14

GAGCGCCGCGCCGCGCGCGCGCGCGCACTGCAGCCCCAGGCCCGGCCCGCCCCACCCACGCTCT
 GCGTTGCTGCCCCCGCTGGGCCAGGCCCAAGGCAAGGACAAGCAGCTGTCAAGGAACTT
 CCGCCGGAGTCGAATTTACGTGCAGCTGCCGCAACCAAGGTTCCAAGATGTGGTTTGCGGGG
 GCTTCGCGTGTTCCAAGAACTGCCTGTGCGCCCTCAACCTGCTTTACACCTTGGTTAGTCTG
 CTGCTAAATTGGAATTGCTGCGTGGGGCATTGGCTTCGGGCTGATTTCCAGTCTCCGAGTGGT
 CGGCGTGTCTATTGCAGTGGGCATCTTCTTGTTCCTGATTGCTTTAGTGGGTCTGATTGGAG
 CTGTAAAAACATCATCAGGTGTGCTATTTTTTTTATATGATTATCTGTTACTTGTATTATT
 GTTCAGTTTTCTGTATCTTGCGCTTGTTTAGCCCTGAACCAGGAGCAACAGGGTCAGCTTCT
 GGAGGTTGGTTGGAACAATACGGCAAGTGCTCGAAATGACATCCAGAGAAATCTAAACTGCT
 GTGGGTTCCGAAGTGTTAAACCAATGACACCTGTCTGGCTAGCTGTGTTAAAAGTGACCAC
 TCGTGCTCGCCATGTGCTCCAATCATAGGAGAATATGCTGGAGAGGTTTTGAGATTTGTGG
 TGGCATTGGCCGTGTTCTTCAGTTTTATAGAGAGATCTGGTGATTTGGCTGACCTACAGATA
 GGAACCAAGGAGTCCCGCGCGCAATCTAGTGCATTTCTTTGATGAGAAAAACAGGAAGAT
 TTCCTTTGTAATTATGACTCTTGTTCACTTTCTGTAATTTCTGTTAAGCTCCATTTTGCCAGT
 TTAAGGAAGGAAACATATCTGGAAGTACCTTATTGATAGTGAATTATATATTTTTTACT
 CTATGTTTTCTCTACATGTTTTTTTCTTTCCGTTGCTGAAAAATATTGAAACTTGTGGTCTC
 TGAAGCTCGGTGCGACCTGGAATTTACTGTATTCTATTGTCGGGCACTGTCCACTGTGGCCTT
 TCTTAGCATTTTTTACCTGCGAGAAAACTTTGTATGGTACCACTGTGTTGGTTATATGGTGAA
 TCTGAACGTACATCTCACTGGTATAAATTATGTAGCACTGTGCTGTGTAGATAGTTCCTAC
 TGGAAAAAGAGTGGAATTTATTAAGTACAGAACTATGAGATCTGTTATGTTAAGGGAAA
 TCCAAATCCCAATTTTTTTTGGTCTTTTAGGAAAGATTGTTGTGGTAAAAAGTGTTAGTA
 TAAAAATGATAATTACTTGTAGTCTTTATGATTACACCAATGTAATTCTAGAAATAGTTAT
 GTCTTAGGAAATGTGGTTTAAATTTTGACTTTTACAGGTAAGTGCAAGGAGAAAGTGTTT
 CATGAAATGTTCTAATGTATAATAACATTTACCTTCAGCCTCCATCAGAATGGAACGAGTTT
 TGAGTAATCAGGAAGTATATCTATATGATCTTGATATTGTTTTATAATAATTTGAAGTCTAA
 AAGACTGCATTTTTAAACAAGTTAGTATTAATGCGTTGGCCCCAGTAGCAAAAAGATATTG
 ATTTATCTTAAAAATTGTTAAATACCGTTTTTCATGAAATTTCTCAGTATTGTAAACAGCACTT
 CTCAAACCTAAGCATATTTGAATATGATCTCCATAAATTTGAAATTGAAATCGTATTGTGTG
 GCTCTGTATATTCTGTTAAAAAATTAAAGGACAGAAACCTTTCTTTGTGTATGCATGTTTGA
 ATTAAGAAGAAAGTAATGGAAG

FIGURE 15

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA39979

><subunit 1 of 1, 204 aa, 1 stop

><MW: 22147, pI: 8.37, NX(S/T): 3

MVCGGFACSKNCLCALNLLYTLVSLLLIGIAAWGIGFGLISSLRVVGVIAGIFLFLIALV
GLIGAVKHHQVLLFFYMIILLLVFIVQFSVCACALALNQEQQQLLEVGNNTASARNDIQR
NLNCCGFRSVNPNDTCLASCVKSDHSCSPCAPIIGEYAGEVLRFRVGGIGLFFSFTEILGVWL
TYRVRNQKDPRANPSAFL

Signal Peptide:

amino acids 1-34

Transmembrane domains:

amino acids 47-63, 72-95 and 162-182

FIGURE 16

TGATGGAGCTGTAAAAAANTCTTCAGGTGTTGTNATTTTTTTTATATGATTATTCTGTAANT
TGTATTTATTGTTTCAGTTTTNTGTATCTTGCGCTTGTTTAGCCNTGAACCAGGAGCAACAGG
GTCAGNTTNTGGAGGTTGGTTGGAACAATACGGCAAGTGCTCGAAATGACATCCAGAGAAAT
NTAAACTGCTGTGGGTTCCGAAGTGTTAACCCAAATGACACCTGTNTGGCTAGCTGTGTTAA
AAGTGACCACTNGTGCTCGCCATGTGCTCCAATCATAGGAGAATATGCTGGAGAGGTTTTGA
GATTTGTTGGTGGCATTGGCCTGTTNTTCAGTTTTACAGAGATCCTGGGTGTTTGGCTGACC
TACAGATACAGGAACCAG

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FIGURE 17

AATCCCAAATCCCCAATTTTGGNCTTTTAGGGAAAGATGTGTTGTGGTAAAAAGTGT
TAGTATAAAAATGATAATTTACTTGTAGTCTTTTATGATTACACCAATGTATCTAGAATAG
TTATGTCTTAGGAAATTGTGGTTTAATTTTGACTTTTACAGGTAAGTGCAAAGGAGAAGTG
GTTTCATGAAATGTTCTAATGTATAATAACATTACCTTCAGCCTCCCATCAGAATGGAACG
AGTTTTGAGTAATCCAGGAAGTATATCTATATGATCTTGATATTGTTTTATATAATTTGAAG
TCTAAAAGACTGCATTTTAAACAAGTTAGTATTAATGCGTTGGCCACGTAGCAAAAAGAT
ATTTGATTATCTTAAAAATTGTAAATACCGTTTTTCATGAAAGTTCTCAGTATTGTAACAGC
AACTTGTCAAACCTAAGCATATTTGAATATGATCTCCATAATTTGAAATTGAAATCGTATT
GTGTGGAGGAAATGGCAATCTTATGTGTGCTGAAGGACACAGTAAGAGCACCAAGTTGTGCC
CCACTTGC

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FIGURE 18

ATGATTATTCTGTTACFTGTATTTATTGTTTCAGTTTTATGGTATCTTGC GCTTGTTTAGCCC
CTGA AACCAAGGAGCAACAGGGNNCAGCTTCCTGGAGGTTTGGTTGGCAACAATCACGGCCAAG
TGACTCCGCAAATGACATCCAGAGAAATCCTAAACTGCTGTGGGTTCTCGAAGTGTTAAACC
AAATGACACCTGTCTGCTGCTGCTGTGTTAAAGTGACCACTCTGCTGCTCGCATGTGCTCCAA
TCATAGGAGAAATATGC

[illegible]

FIGURE 19

CAGTCACCATGAAGCTGGGCTGTGTCCTCATGGCCTGGGCCCTCTACCTTTCCTTGGTGTG
CTCTGGGTGGCCAGATGCTACTGGCTGCCAGTTTTGAGACGCTGCAGTGTGAGGGACCTGT
CTGCACTGAGGAGAGCAGCTGCCACACGGAGGATGACTTGACTGATGCAAGGGAAGCTGGCT
TCCAGGTCAAGGCTACACTTTCAGTGAACCTTCCACCTGATTGTGTCCTATGACTGGCTG
ATCCTCCAAGGTCAGCCAAGCCAGTTTTGAAGGGGACCTGCTGGTCTCGCGCTGCCAGGC
CTGGCAAGACTGGCCACTGACTCAGGTGACCTTCTACCGAGATGGCTCAGCTCTGGGTCCCC
CCGGGCTTAACAGGGAATTCTCCATCACCGTGGTACAAAAGGCAGACAGCGGGCACTACCAC
TGCAGTGGCATCTTCCAGAGCCCTGGTCTGGGATCCCAGAAAACAGCATCTGTTGTGGCTAT
CACAGTCCAAGAACTGTTTTCAGCGCCAATTCTCAGAGCTGTACCCTCAGCTGAACCCCAAG
CAGGAAGCCCCATGACCTGAGTTGTGACACAAAGTTGCCCTGCAGAGGTGAGCTGCCGCG
CTCCTCTTCTCCTTCTACAAGGATGGAAGGATAGTGCAAAGCAGGGGGCTCTCCTCAGAATT
CCAGATCCCCACAGCTTCAGAAGATCACTCCGGGTCACTACTGGTGTGAGGCAGCCACTGAGG
ACAACCAAGTTTGGAAAACAGAGCCCCAGCTAGAGATCAGAGTGCAGGGTGCTTCCAGCTCT
GCTGCACCTCCCACATTGAATCCAGCTCCTCAGAAATCAGCTGCTCCAGGAACCTGCTCCTGA
GGAGGCCCCCTGGGCTCTGCCTCCGCCGCCAACCCATCTTCTGAGGATCCAGGCTTTTCTT
CTCCTCTGGGGATGCCAGATCCTCATCTGTATCACCAGATGGGCCTTCTTCTCAAACATG
CAGGATGTGAGAGTCTCCTCGGTCACTGCTCATGGAGTTGAGGGAATTATCTGGCCACCA
GAAGCCTGGGACCACAAAGGCTACTGCTGAATTAGAAGTAACAGTTTCATCCATGATCTCACT
TAACCAACCCAAATAAATCTGATTCTTTATTTTCTCTTCTGTCTGTCACATATGCATAAGTA
CTTTTACAAGTTGTCCCAGTGTTTTGTTAGAATAATGTAGTTAGGTGAGTGTAATAAATTT
ATATAAAGTGAGAATTAGAGTTTAGCTATAAATGTGTATTCTCTCTTAACACAACAGAATTC
TGCTGTCTAGATCAGGAATTTCTATCTGTTATATCGACCAGAAATGTTGTGATTTAAAGAGAA
CTAATGGAAGTGATTGAATACAGCAGTCTCAACTGGGGCAATTTTGCCCCCAGAGGACA
TTGGGCAATGTTTGGAGACATTTTGGTCATTACTTGGGGGGTTGGGGGATGGTGGGATGT
GTGTCTACTGGCATCCAGTAAATAGAAGCCAGGGGTGCCGCTAAACATCCTATAATGCACAG
GGCAGTACCCCCAACGAAAAATAATCTGGCCAAAAATGTCAGTTGTACTGAGTTTGAGAAA
CCCCAGCCTAATGAACCCCTAGGTGTTGGGCTCTGGAATGGGACTTTGTCCCTTCTAATTAT
TATCTCTTCCAGCCTCATTGAGCTATTCTTACTGACATACCAGTCTTTAGCTGGTGTCTATG
GTCGTCTCTTTAGTTCAGTTTGTATCCCTCAAAGCCATTATGTTGAAATCCTAATCCCC
AAGGTGATGGCATTAGAAGTGGGCCCTTGGGAAGTGATTAGATCAGGAGTGCAGAGCCCTC
ATGATTAGGATTAGTGCCCTTATTATAAAAGGCCCCAGAGAGCTAACTACCCCTTCCACCAT
ATGAGGACGTGGCAAGAAGATGACATGTATGAGAACCAAAAAACAGCTGTGCGCAAACACCG
ACTCTGCTGTTGCCTTGATCTTGAACCTCCAGCCTCCAGAACTATGAGAAATAAAATCTGG
TTGTTTGTAGCCTAA

40204.102401

FIGURE 20

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA40594

><subunit 1 of 1, 359 aa, 1 stop

><MW: 38899, pI: 5.21, NX(S/T): 0

MKLGCVLMAWALYLSLGLVWVAQMLLAASFETLQCEGFPVCTEESCHTEDDLTDAREAGFQV
KAYTFSEPFHLIVSYDWLILQGPAKPVFEGDLLVLRCAWQDWPLTQVTFFYRDGSALGPPGP
NREFSITVVQKADSGHYHCSGIFQSPGPGIPETASVVAITVQELFPAPILRAVPSAEFQAGS
PMTLSCQTKLPLQRSAAARLLFSFYKDGRIVQSRGLSSEFQIPTASEDHSGSYWCEAATEDNQ
VWKQSPQLEIRVQGASSSAAPPTLNPAPQKSAAPGTAPEEAPGPLPPPTPSSDPGFSSPL
GMPDPHLYHQMGLLLKHMQDVRVLLGHLLMELRELSGHQKPGTTKATAE

Signal sequence:

amino acids 1-17

Leucine zipper pattern sequence:

amino acids 12-33

Protein kinase C phosphorylation site:

amino acids 353-355

FIGURE 21

CCCACGCGTCCGCCACGCGTCCGCCACGCGTCCGCCACGCGTCCGGGCCACCAGAAGTT
TGAGCCTCTTTGTAGCAGGAGGCTGGAAGAAAGACAGAAGTAGCTCTGGCTGTGATGGGG
ATCTTACTGGGCCTGCTACTCCTGGGGCACCTAACAGTGGACACTTATGGCCGTCCCATCCT
GGAAGTGCCAGAGAGTGAACAGGACCTTGGAAAGGGATGTGAATCTTCCCTGCACCTATG
ACCCCTGCAAGGCTACACCAAGTCTTGGTGAAGTGGCTGGTACAACGTGGCTCAGACCT
GTCACCATCTTTCTACGTGACTCTTCTGGAGACCATATCCAGCAGGCAAGTACCAGGGCCG
CCTGCATGTGAGCCACAAGGTTCCAGGAGATGTATCCCTCCAATTGAGCACCTGGAGATGG
ATGACCGGAGCCACTACACGTGTGAAGTCACCTGGCAGACTCCTGTATGGCAACAGTCTGTG
AGAGATAAGATTACTAGCTCCGTGTCCAGAACTCTCTGTCTCCAAGCCACAGTGACAC
TGGCAGCGGTTATGGCTTCACGGTGCCCCAGGGAATGAGGATTAGCCTTCAATGCCAGGCTC
GGGGTTCTCCTCCCATCAGTTATATTTGGTATAAGCAACAGACTAATAACCCAGGAACCCATC
AAAGTAGCAACCCCTAAGTACCTTACTCTTCAAGCCTGCGGTGATAGCCGACTCAGGCTCCTA
TTTCTGCACTGCCAAGGGCCAGGTTGGCTCTGAGCAGCACAGCGACATTGTGAAGTTTGTGG
TCAAAGACTCCTCAAAGCTACTCAAGACCAGACTGAGGCACCTACAACCATGACATACCCC
TTGAAAGCAACATCTACAGTGAAGCAGTCCCTGGGACTGGACCACTGACATGGATGGCTACCT
TGGAGAGACCAGTGCTGGGCCAGGAAAGAGCCTGCCTGTCTTTGCCATCATCCTCATCATCT
CCTTGTGCTGTATGGTGGTTTTTACCATGGCCTATATCATGCTCTGTGCGAAGACATCCCAA
CAAGAGCATGTCTACGAAGCAGCCAGGTTAAGAAAGTCTCTCCTCTTCCATTTTTGACCCCGT
CCCTGCCCTCAATTTTTGATTACTGGCAGGAAATGTGGAGGAAGGGGGTGTGGCACAGACCC
AATCCTAAGGCCGGAGGCCCTTCAAGGTCAGGACATAGCTGCCTTCCCTCTCTCAGGCACCT
CTGAGGTTGTTTTGGCCCTCTGAACACAAAGGATAATTTAGATCCATCTGCCTTCTGCTTCC
AGAATCCCCTGGGTGGTAGGATCCTGATAATTAATTGGCAAGAATTGAGGCAGAAGGGTGGGA
AACCAGGACACAGCCCCAAGTCCCTTCTTATGGGTGGTGGGCTCTTGGGCCATAGGGGACA
TGCCAGAGAGGCCAACGACTCTGGAGAAACCATGAGGGTGGCCATCTTCGCAAGTGGCTGCT
CCAGTGATGAGCCAACTTCCAGAATCTGGGCAACAACACTACTCTGATGAGCCCTGCATAGGA
CAGGAGTACCAGATCATGCCCAGATCAATGGCAACTACGCCCCGCTGCTGGACACAGTTCC
TCTGGATTATGAGTTTCTGGCCACTGAGGGCAAAAGTGTCTGTTAAAAATGCCCATTAGGC
CAGGATCTGCTGACATAATTGCCTAGTCAGTCTTGCCTTCTGCATGGCCTTCTTCCCTGCT
ACCTCTCTTCTGGATAGCCAAAGTGTCCGCCCTACCAACACTGGAGCCGTGGGAGTCACT
GGCTTGGCCTGGAATTTGCCAGATGCATCTCAAGTAAGCCAGCTGCTGGATTGGCTCTGG
GCCCTTCTAGTATCTCTGCCGGGGCTTCTGGTACTCCTCTCTAAATACCAGAGGGAAGATG
CCCATAGCACTAGGACTTGGTCATCATGCCTACAGACACTATTCAACTTTGGCATCTTGCCA
CCAGAAGACCCGAGGGAGGCTCAGCTCTGCCAGCTCAGAGGACCGCTATATCCAGGATCAT
TTCTCTTCTTTCAGGGCCAGACAGCTTTTAATTGAAATTGTTATTTACAGGCCAGGGTTCA
GTTCTGCTCCTCCACTATAAGTCTAATGTTCTGACTCTCTCCTGGTGTCTAATAAATATCTA
ATCATAACAGC

FIGURE 22

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45416

><subunit 1 of 1, 321 aa, 1 stop

><MW: 35544, pI: 8.51, NX(S/T): 0

MGILLGLLLLLGHLLTVDTYGRPILEVPESVTGPWKGVDVNLPCITYDPLQGYTQVLVKWLVRGS
DPVTIFLDRSSGDHIQQAKYQGRHLVSHKVPBGDVSLLQLSTLEMDDRSHYTCEVTWQTPDGNQ
VVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQGMRLSLQCQARGSPPISYIWKQQTNNQE
PIKVATLSTLLFKPAVIADSGSYFCTAKGQVGSEQHSDIVKFVVKDSSKLLKTKTEAPTMT
YPLKATSTVKQSWDWTDMGYLGETSAGPGKSLPVFAILLIISLCCMVVFTMAYIMLCRKT
SQQEHVYEAAAR

Signal Sequence:

amino acids 1-19

Glycosaminoglycan attachment site:

amino acids 149-152

Transmembrane domain:

amino acids 282-300

FIGURE 23

GCGCCGGGAGCCCATCTGCCCCAGGGGCACGGGGCGCGGGGCCGGCTCCCGCCCGGCACAT
GGCTGCAGCCACCTCGCGCGCACCCCGAGGCGCCGCGCCAGCTCGCCCGAGGTCCTGCGGA
GGCGCCCGGCGCGCCCGGAGCCCAAGCAGCAACTGAGCGGGGAAGCGCCCGCTCGCGGGATC
GGGATGTCCCTCTCCTCTCTCTCTCTGCTAGTTTCCCTACTATGTTGGAAACCTTGGGGACTCA
CACTGAGATCAAGAGAGTGGCAGAGGAAAAGGTCAC'TTGGCCCTGCCACCATCAACTGGGGC
TTCCAGAAAAAGACACTCTGGATATTGAATGGCTGCTCACCGATAATGAAGGGAACCAAAAA
GTGGTGATCACTTACTCCAGTCGTCACTGTCTACAATAACTTGACTGAGGAACAGAAGGGCCG
AGTGGCCTTTGCTTCCAAATTTCTGGCAGGAGATGCCTCCTTGCAGATTGAACCTCTGAAGC
CAGTGTATGAGGCGCGTACACCTGTAAAGTTAAGAATTCAAGGCGCTACGTGTGGAGCCAT
GTCATCTTAAAGTCTTAGTGAGACCATCCAAGCCCAAGTGTGAGTTGGAAGGAGAGCTGAC
AGAAGGAAGTGACCTGACTTTGCAGTGTGAGTCATCCTCTGGCAGAGAGCCCATTTGTGTATT
ACTGGCAGCGAATCCGAGAGAAAGAGGGAGAGGATGAACGCTCTGCCTCCCAAATCTAGGATT
GACTACAACCACTCTGGACGAGTTCTGCTGCAGAATCTTACCATGTCCTACTCTGGACTGTA
CCAGTGCACAGCAGGCAACGAAGCTGGGAAGGAAAGCTGTGTGGTGCGAGTAAGTGTACAGT
ATGTACAAAGCATCGGCATGGTTGACAGGAGCAGTGACAGGCATAGTGGCTGGAGCCCTGCTG
ATTTTCTCTTGTGTGGCTGCTAATCCGAAGGAAAGACAAAGAAAGATATGAGGAAGAAGA
GAGACCTAATGAAATTCGAGAAGATGCTGAAGCTCCAAAGCCCGTCTTGTGAAACCCAGCT
CCTCTTCTCAGGCTCTCGGAGCTCACGCTCTGGTTCTTCTCCACTCGCTCCACAGCAAT
AGTGCTCAGCGAGCCAGCGGACACTGTCAACTGACGCAGCACCCAGCCAGGGCTGGCCAC
CCAGGCATACAGCCTAGTGGGCCCAGAGGTGAGAGGTTCTGAACCAAAGAAAGTCCACCATG
CTAATCTGACCAAAGCAGAAACCAACCCAGCATGATCCCCAGCCAGAGCAGAGCCTTCCAA
ACGGTCTTGAATTACAATTGAGCTTGACTCCACGCTTTCCTAGGAGTGACGGGTCTTTGGACTC
TTCTCGTCATTGGAGCTCAAGTCACCAGCCACAAACCATGAGAGGTCACTCAAGTAGCA
GTGAGCATTGCACGGAACAGATTAGATGAGCATTTTCCCTTATACAATACCAACCAAGCAAA
AGGATGTAAGCTGATTCACTCTGTAAAAAGGCATCTTATTGTGCTTTAGACCAGAGTAAGGG
AAAGCAGGAGTCCAAATCTATTTGTTGACCAGGACCTGTGGTGAGAAGGTTGGGGAAAGGTG
AGGTGAATATACCTAAACTTTTAAATGTGGGATATTTGTATCAGTGTCTTGTATTACAATT
TTCAAGAGGAAATGGGATGCTGTTTGTAAATTTCTATGCATTTCTGCAAACTTATTGGATT
ATTAGTTATTAGACAGTCAAGCAGAACCCACAGCCTTATTACACCTGTCTACACCATGTAC
TGAGCTAACCACTTCTAAGAACTCCAAAAAGGAAACATGTGTCTTCTATTCTGACTTAACT
TTCATTTGTATAAGGTTTGGATATTAATTTCAAGGGAGTTGAAATAGTGGGAGATGGAGA
AGAGTGAATGAGTTTCTCCCACTCTATACTAATCTCACTATTGTATTAGGCCCAAAATAAC
TATGAAAGGAGACAAAAATTTGTGACAAAGGATTGTGAAGAGCTTTCCATCTTCTATGATT
ATGAGGATTGTTGACAAACATTAGAAATATATAATGGAGCAATTGTGGATTTCCTCTCAAAT
CAGATGCCTCTAAGGACTTTCCTGCTAGATATTTCTGGAAGGAGAAAAATACAACATGTCAATT
TATCAACGTCCTTAGAAAGAAATTTCTTAGAGAAAAAGGATGCTGAAATGCTGAAAGATT
CCCAACATACCATATAGTCTCTTCTTTCTGAGAAATGTGAACCAAGAAATTGCAAGACTGG
GTGGACTAGAAAGGAGATTAGATCAGTTTTCTCTTAATATGTCAAGGAAGGTAGCCGGGCA
TGGTGCCAGGCACCTGTAGGAAAAATCCAGCAGGTGGAGGTTGCAGTGAGCCGAGATTATGCC
ATTGCACTCCAGCCTGGGTGACAGAGCGGGACTCCGTCTC

FIGURE 24

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45419

><subunit 1 of 1, 373 aa, 1 stop

><MW: 41281, pI: 8.33, NX(S/T): 3

MSLLLLLLLLVSYVGTGLGTHTEIKRVAEEKVTLPCHHQLGLPEKDTLDIEWLLTDNEGNQKV
VITYSSRHVYNNLTTEEQKGRVAFASNFLAGDASLQIEPLKPSDEGRYTCKVKNSGRYVWSHV
ILKVLVRPSKPKCELEGELTEGSDTLQCESSSGTEPIVYYWQRIREKEGEDERLPPKSRID
YNHPGRVLLQNLMTSYSGLYQCTAGNEAGKESCVRVTVQYVQSIGMVAGAVTGIVAGALLI
FLLVWLLIRRKDKERYEEEEERPNEIREDAEAPKARLVKPSSSSSGSRSSRSGSSSTRSTANS
ASRSQRTLSTDAAPQPLATQAYSLVGPEVRGSEPKKVHHANLTKAETTPSMIPSQSRAFQTV

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 232-251

FIGURE 25

GTCGTTCCCTTTGCTCTCTCGCGCCAGTCCTCCTCCCTGGTTCTCCTCAGCCGCTGTGCGGAGGAGCACC CGGA
 GAGCGCGGGCTCAGTGC GCGCGGGCTTCTCCCGCCTGGGCGGCTCGCGCGCTGGGCAGGTGCTGAGCGCCCTAG
 AGCCTCCCTTGGCGCCTCCTCTCTGCGCGCCGACAGTCACATGGGGTTGTTGAGGTAGATGGGCTCCCG
 GCGCGGGAGGCGCGGTGGATGCGCGCTGGGCAGAACGAGCCGCCGATTCTCAGCTGCCCCGCGCGCCCCGGGGC
 CCCCCTGCGAGTCCCCGGTTTCAGCCATGGGGACCTCTCCGAGCAGCAGCACCGCCCTCGCCTCTCTGAGCCGCATC
 GCCCGCGGAGCCACAGCCACGATGATCGCGGGCTCCTCTCTCTGCTTGGATTTCCTTAGCACCAACACAGCTCAG
 CCAGAACAGAGGCTTCGAATCTCATTTGGCACATACCGGCATGTTGACCCGTGCCACCGGCCAGGTGCTAACCTGT
 GACAAAGTCTTCAGCAGGAACCTTATGCTCTGAGCACTGTATACCAACACAGCCTGCGCGCTCTGCAAGCTTGCCCT
 GTGGGGGTTTACCCAGCATGAGAAATGGCATAGAGAAATGCCATGACTGTATGACCCATGCCCCATGGCCAAATG
 ATTGAGAAATTTACCTGTGTGCTCTGACTGACCGAGAAATGCACTTGCCCACTGGCATGTTCCAGTCTAACGCT
 ACCTGTGGCCCTACACGCTGTGTCTCTGTGGGTTGGGTTGCGGAGAAAGGGAAGAGACTGGAGATGTGCGG
 TGTAAAGCACTGTCTCGGGTACCTTCTCAGATGTGCTCTTAGTGTGATGAAATGCCAAGCATACACAGACTGT
 CTGAGTCAGAACCTGTGTGTGATCAAGCGGGGACCAAGGAGACAGAACAGTCTGTGGGCACACTCCGCTCCTTC
 TCCAGCTCCACCTCACCCTTCCCTGGCACAGCCATCTTCCACGCCCTGAGCACATGGAAACCCATGAAGTCCCT
 TCCTCCACTTATGTTCCCAAGGCGATGAACCTCAACAGAAATCCAACCTCTCTGCTCTCTGTTAGACCAAGGTA
 AGTAGCATCCAGGAAGGGGACCTCTGACACACAGCTCAGCAAGGGGGAAGGAAGCGTGAAACAAGACCTC
 CCAACCTCTCAGGTAGTCAACCAACAGCAGAGGCCCCACCAACAGACATCTCTGAAGCTGCTCCGCTCCATGGAG
 GCGACTGGGGGAGGAGAGTCCAGCACGCCCATCAAGGGGCCCAAGAGGGGACATCTAGACAGCTTCAACAG
 CATTTTGACATCAATGAGCATTTGCCCTGGATGATTTGTCTTTTCTGCTGTGGTGCTTGTGGTGATTGTGGTG
 TGCAGTATCCGGAAGAGCTCGAGGACTCTGAAAAAGGGGCCCGGCGAGGATCCCACTGCCATTGTGGAAGGCA
 GGGCTGAAGAAATCCATGACTCCAACCGAGAACCGGGAGAAATGGATCTACTACTGCAATGGCCATGGTATCGAT
 ATCCTGAAGCTTTGTAGCAGCCCAAGTGGGAAGCCAGTGGAAAGATATCTATCAGTTTCTTGTGAATGCCAGTGAG
 AGGGAGGTGTCTGCTTTTCTCAATGGGTACACAGCCGACCAAGAGCGGGCTTACGCACTCTGCAGCACTGGACC
 ATCCGGGGCCCCGAGGCCAGCTCGCCAGCTAATTAGCGCCTCGCGCAGCACCGGAGAAACGATGTTGTGGAG
 AAGATTCTGTGGCTGTATGGAAGACACACCCAGCTGGAATGACAACTAGCTCTCCGATGAGCCCCAGCCCG
 CTTAGCCCGAGCCCCATCCCGAGCCCCAACGCGAACTTGAGAATTCGCTCTCTGAGCGTGGAGCCTTCCCA
 CAGGAACAAGAACAGGGCTTCTCTGTGATGAGTGGAGCCCTTCTCCGCTGTGACTCTACATCCAGCGGCTCC
 TCCGCGCTGAGCAGGAACGGTTCCTTTATACCAAGAAAAAGAGGACACAGTGTTCGCGGAGGTACGCTGGAC
 CCTGTGACTTGCAGCTATCTTTGATGACATGCTCCACTTTCTAAATCTCAGGAGCTGCGGGTGATTGAAGAG
 ATTCCCGAGGCTGAGGACAACTAGACCGGCTATTGCAAAATATTGGAGTCAAGAGCCAGGAAGCCAGCCAGACC
 CTCTGGACTCTGTTTATAGCCATCTTCTGACCTGCTCTAGAACATAGGGAATCTGCAATCTGGAATATTACTCA
 ATTAGTGGCAGGTGGTTTTTAATTTCTCTCTGTTTCTGATTTTGTGTTTGGGGTGTGTGTGTGTGTGTGTGT
 GT
 TCTCTCTCTTTTTTTAAATAACTCTCTGCGGAAGTTGGTTTAAAGCTTTGCCACATGTAACGTGTGTGTGTGAA
 ATACCCACCATTAAGTTTTTTTAAATGTCATATTTCTCCATTTTGCCTCTCTATGATTTTCAAGATTAATCTG
 TGCACTTTAAATTTACTTAATACATATAATGCAATGCACTGTAATTTTCCCAACATGGAATGTGAGGCTCTTAAC
 TTTCTAAAGATTAATGGCACTCTGTGAATCTTATAAGCAGTCTTTATGTCTTTAAACATCACACTACTTTTT
 AAAACCAATATATTACTATTTTATATTGTTGTGCTTTATAAATTTTCTTAAAGATTAAAGAAATTAAGAA
 CCCATTTGAGTTACTGTAATGCAATTCACCTTGAGTTATCTTTTAAATATGTCTGTATAGTTTCAATTTACCTGG
 CTGAAACTTGACCACTATTTGCTGATTTGATGGTTTTCACTGGACACCGTGTAGAACTCTGATTTACTGTTGAT
 TCTCTTATGCTAATATGCTCTGGGCTGGAGAAATGAAATCTCAAGCCATCAGGATTTGCTATTTTAAGTGCGCT
 GACAACTGGGCCACCAAGAACTTGAATCTCACCTTTAGGATTTAGAGTTGTGGAACACATTTGCTGCACTTT
 GGAAGTCAAAATCAAGTCCGAGTGGCGCCCTTTCCATAGAGAAATTTGCCAGCTTTGCTTTAAAGATGTCTTG
 TTTTATATACACATTAATCAATAGGTCCAATCTGCTCTCAAGGCCCTTGGTCTCGTGGGGAATCTCTTACCAAT
 ACTTTAATTAAGAAATGGTGCACCTGTAAGACCTTGTCTGATATTTGTGCAACTATGCTCCCAATTAAGAAAT
 TACCTTCTAATGCTCAGTTGCGAGGTTCCAATGCAAGGTGCGCTGGACTCCCTTTGTGTGGGTGGGGTTGTGG
 GTAGTGTGAAGCGCATATCAGAAAAATGCTTCAAGTGTACTAATTTATTAATAAACATTAGGTGTTGTGTA
 AAAAAAAAA

GTCGTTCCCTTTGCTCTCTCGCGCCAGTCCTCCTCCCTGGTTCTCCTCAGCCGCTGTGCGGAGGAGCACC CGGA

FIGURE 26

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52594

><subunit 1 of 1, 655 aa, 1 stop

><MW: 71845, pI: 8.22, NX(S/T): 8

MGTSPPSSSTALASCSRIARRATATMIAGSLLLLGFLSTTTAQPEQKASNLIGTYRHVDRATG
QVLTCDKCPAGTYVSEHCTNTSLRVCSSCPVGTFTTRHENGIEKCHDCSQPCPWPMEIKLPCA
ALTDRECTCPPGMFQSNATCAPHTVCPVGWGVRRKGTETEDVRCKQCARGTFSDVPSSVMKC
KAYTDCLSQNLVVIKPGTKETDNVCGLPSFSSSTSPSPGTAIFRPEHMETHEVPSSTYVP
KGMNSTESNSSASVRPKVLSSIQEGTVPDNTSSARGKEDVNKTLPNLQVNVHQGGPHHRHIL
KLLPSMEATGGEKSSTPIKGPKRGHPRQNLHKHFDINEHLPWMIVLFLLLVLVVIIVVCSIRK
SSRTLKKGPRQDPSAIVEKAGLKKSMPTQNREKWIYYCNGHGIDILKLVAQVGSQWKDIY
QFLCNASEREVAAFSNGYTADHERAYAALQHWITIRGEASLAQLISALRQHRNRNDVVEKIRG
LMEDTTQLETDKLALPMSPLSPSPSPNAKLENSALLTVEPSQDKNGGFFVDESEPLL
RCDSTSSGSSALSRRNSFITKEKDTVLRQVRLDPCDLQPIFDDMLHFLNPEELRVIEEIPQ
AEDKLDRLFEIIGVKSQEASQTLLDSVYSHLPDLL

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 350-370

FIGURE 27

ATGGGAAGCCAGTAACACTGTGGCCTACTATCTCTTCOGTGGTGCCATCTACATTTTGGGA
CTCGGGAATATGAGGTAGAGGTGGAGGCGGAGCCGGATGTCAGAGGTCCTGAAATAGTCAC
CATGGGGGAAAAATGATCCGCCTGCTGTTGAAGCCCCCTTCTCATTCGGATCGCTTTTGGGCC
TTGATGATTTGAAAAATAAGTCTGTGCAACAGATGCAGATGCTGTTGCTGCACAGATCCTG
TCACTGCTGCCATTGAAGTTTTTTCCAATCATCGTCATTGGGATCATTGCAATTGATATTAGC
ACTGGCCATTGGTCTGGGCATCCACTTCGACTGCTCAGGGAAGTACAGATGTCGCTCATCCT
TTAAGTGTATCGAGCTGATAGCTCGATGTGACGGAGTCTCGGATTGCAAAGACGGGGAGGAC
GAGTACCGCTGTGTCCGGGTGGGTGGTCAGAAATGCCGTGCTCCAGGTGTTCCAGAGTGCCTTC
GTGGAAGACCATGTGCTCCGATGACTGGAAGGGTCACTACGCCAATGTTGCCCTGTGCCCAAAC
TGGGTTTCCCAAGCTATGTGAGTTAGATAACCTCAGAGTGAGCTCGCTGGAGGGGCGAGTTC
CGGGAGGAGTTTGTGTCCATCGATCACCTCTTGCCAGATGACAAGGTGACTGCATTACACCA
CTCAGTATATGTGAGGGAGGGATGTGCCTCTGGCCACGTGGTTACCTTCAGTGCCACAGCCT
GTGGTTCATAGAAGGGGTACAGCTCACGCATCGTGGGTGGAACATGTCTTGTCTCTCGCAG
TGGCCCTGGCAGGCCAGCCTTCAGTTCAGGGCTACCACTGTGCGGGGGCTCTGTCTATCAC
GCCCTGTGGATCATCTAGCTGCACACTGTGTTTATGACTGTGACCTTCCCAAGTCATGGA
CCATCCAGGTGGTCTAGTTTCCCTGTTGGACAATCCAGCCCCATCCCACTTGGTGGAAG
ATTGTCTACCACAGCAAGTACAAGCCAAAGAGGCTGGGCAATGACATCGCCCTTATGAAGCT
GGCCGGGCCACTCACGTTCAATGAAATGATCCAGCCTGTGTGCCTGCCCAACTCTGAAGAGA
ACTTCCCCGATGGAAAAGTGTGCTGGACGTGAGGATGGGGGGCCACAGAGGATGGAGGTGAC
GCCTCCCTGTCTTGAACCACGCGGCGTCCCTTTGATTTCACAAAGATCTGCAACCCACAG
GGACGTGTACGTTGGCATCATCTCCCCCTCCATGCTCTGCGCGGGCTACCTGACGGGTGGCG
TGGACAGCTGCCAGGGGGACAGCGGGGGGCCCTGGTGTGTCAAGAGAGGAGGCTGTGGAAG
TTAGTGGGAGCGACAGCTTTGGCATCGGCTGCGCAGAGGTGAACAAGCTCGGGGTGTACAC
CCGTGTCACTCTCTTCTGGACTGGATCCACGAGCAGATGGAGAGAGACCTAAAAACCTGAA
GAGGAAGGGGACAAGTAGCCACCTGAGTTCCCTGAGGTGATGAAGACAGCCCGATCCCTCCCT
GGACTCCCCTGTAGGAACCTGCACACGAGCAGACACCCCTTGGAGCTCTGAGTTCGGCACCA
GTAGCAGGCCCCGAAAGAGGCACCTTCCATCTGATTCCAGCACAACTTCAAGCTGCTTTT
GTTTTTGTTTTTTTGAGGTGGAGTCTCGCTCTGTTGCCAGGCTGGAGTGACGTGGCGAAA
TCCCTGCTCACTGCAGCCTCCGCTTCCCTGGTTCAAGCGATTCTCTTGCTCAGCTTCCCCA
GTAGCTGGGACCACAGGTGCCCGCCACCACACCCAACTAATTTTTGTATTTTAGTAGAGAC
AGGGTTTCAACATGTTGGCCAGGCTGCTCTCAAACCCCTGACCTCAAATGATGTGCCTGCTT
CAGCCTCCCACAGTGCTGGGATTACAGGCATGGGCCACCACGCCTAGCCTCAGCTCCTTTC
TGTCTTCACTAAGAACAAAAGAAGCAGCAACTTGCAAGGGCGGCCTTTCCCACTGGTCCAT
CTGGTTTTCTCTCCAGGGTCTTGCAAAATTCTGACGAGATAAGCAGTTATGTGACCTCAG
TGCAAAGCCACCACAGCCTCAGAAAAGACGACCCAGCCGAAAGTGACAGAACTGCAGT
ACTGCAGCTTTTTCATCTCTTAGGGACCAAGAACCCACCCCTTCTACTTCCAAGACTTAT
TTTACATGTGGGGAGGTTAATCTAGGAATGACTCGTTTAAAGGCTATTTTCATGATTTCTT
TGTAGCATTTGTGCTTGACGTATTATTGTCCTTTGATTCCAATAATATGTTTCTTCCCT
CATGTGCTGGCGTGTCTGCGTGGACTGGTGACGTGAATCAAATCATCCACTGAAA

FIGURE 28

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45234

><subunit 1 of 1, 453 aa, 1 stop

><MW: 49334, pI: 6.32, NX(S/T): 1

MGENDPPAVEAPFSFRSLFGLDDLKISPVAPDADAVAAQILSLLPLKFFPIIVIGIIALILA
LAIGLGIHFDCSGKYRCRSSFKCIELIARCDGVSDCKGEDEYRCVRVGGQNAVLQVFTAAS
WKTMCSDDWKGHYANVACAQLGFPSYVSSDNLRVSSLEGQFREEFVSIHLLPDDKVLTALHH
SVYVREGCASGHVVTLQCTACGHRRGYSSRIVGGNMSLLSQWPWQASLQFGYHLCGGSVIT
PLWIITAAHCVDYDLYLPKSWTIQVGLVSLDNPAPSHLVEKIVYHSKYKPKRLGNDIALMKL
AGPLTFNEMIQPVCLPNSEENFPDGKVCWTSGWGATEDGGDASPVLNHAAVPLISNKICNHR
DVGGGIISPSMLCAGYLTGGVDSCQGDSGGPLVCQERRLWKLVGATSFYGIGCAEVNKPGVYT
RVTSFLDWIHEQMERDLKT

Signal Peptide:

amino acids 1-20

Transmembrane domain:

amino acids 240-284

FIGURE 29

CCCACGCGTCCGCTCTAGTCCCGGGCCAACTCGGACAGTTTGCTCATTATTGCAACGGTCAAGGCTGGCTTGT
 GCCAGAACGGCGCGCGCGCGCACGACGCACACACACGCGGGGGAAACTTTTTTAAAAATGAAGGCTAGAAAGA
 GCTCAGCGCGCGCGCGGGCGCTGCGCGAGGGCTCCGGAGCTGACTCGCCGAGGCGAGGAATCCCTCCGCTCGCGA
 CGCCCGGCGCCCGGCTCGGCGCCCGCGTGGATGGTGCAGCGCTCGCCGCGGGCCGAGAGCTGCTGCATCGTAAG
 GCGCGGACGATGGCAGCGCGCCCGCTGCCCGTGTCCCGCGCCGCGCCCTCTGCTCGCCCTTGGCGCGTGTCTGT
 GCTCGCGCCCTGCGAGGCGCGAGGGGTGAGCTTTATGGAAACCAAGGAAGAGCTGATGAAGTGTGTCAGTGCTCTGT
 TCGGATGGGGACCTCTGGATCCGATGAAAGACTTCGACTCCAAGAATCATCCAGAAGTGTCTGAATATTCCGACT
 ACAACGGGAAGCAAGAACTGATCATATAATCTGGAAGAAAGTAAGGTCTCATTTCCAGCAGTTCACGGGAAC
 CCACATCTGCAAGACCGTATGATGTCTCCCTCGCTCGAAATACACGGGTCACTGTTATACCATGACATGT
 ACGGGATATTCTGATTGACAGCTGACTCTCAGCAGCTGTCTGCTCTCAGGGGACTTAITGTGTTTGAATAATGA
 AAGCTATGCTTTAGAACCAATGAAAGTGACCAACCAAGATACAACTCTTTCCACGAGGAAGCTGAAAGCGT
 CCGGGATCATGTGGATCACATCACAAACACCAAACTCGCTGCAAGAATGTGTTCCACCACTCTCTCAGAC
 ATGGGCAAGAGGCGATAAAGAGAGACCTCAAGGCAACTAAGTATGTGGAGCTGTGTGATCGTGGCAGACAACCG
 AGAGTTTTCAGAGGCAAGGAAAGATCTGGAAGAAAGTTAAGCAGCGATTAAATAGAGATTGCTAATCAGCTTGACAA
 GTTTTACAGACCACTGAACATTCGGATCGGTGTGGTAGCGGTGGAAGTGTGGAATGACATGGACAATGCTCTGT
 AAGTCAGGACCCATTACACAGCTCCATGAATTTCTGGACTGGAGGAAGTGAAGCTTCTACCTCGCAAAATCCCA
 TGACATGCGCAGCTGTGAGTGGGGTTTATTTCAGGGGACCACTCGGCATGCCCCCAATCATGAGCATGTG
 CACGGCAGACCACTGCGGGGAATTGTCAITGACCAATTCAGACAATCCCCCTGGTGCAGCGGTGACCTGGGCACA
 TGAGCTGGGCCACAATTTCCGGATGAATCATGACACACTGGACAGGGCTGTAGCTGTCAAATGGCGGTGAGAA
 AGGAGGCTGCATCATGAACGCTTCCACGGGTACCCATTCCCATTGGTTCAGCAGTTGACAGGGAAGGACTT
 GGAGACCAAGCTTGAGAAAGGAATGGGGGTGTGCTGTTTAACTGCCGGAAGT CAGGGAGTCTTTCCGGGGCCA
 GAAGTGTGGGAACAGATTTGTGGAAGAAGGAGGAGGTGTGACTGTGGGGAGCCAGAGGAATGTATGAATCGCTG
 CTGCAATGCCACCACTGTACCTGAAGCCGAGCGTGTGTGCGCACATGGGCTGTGCTGTGAAGACTGCCAGCT
 GAAGCTGTCAGGAACAGCGTGCAGGGACTCCAGCAACTCTGTGACTCCAGAGTTCTGCAACAGGGGCCAGCCC
 TCACTGCCAGCCAAATGTGTACTCTGCAGATGGGCATCATGTGAGGATGTGGAAGGCTTCTGCTACAATGGCAT
 CTGCCAGACTCAGGAGCAGCATGTGTGACGCTCTGGGGACCAAGTGTCAAAGCTGCCCTGGGATCTGCTTGA
 GAGAGTCAATTTCTGAGGTGATCTTATGGCAACTGTGGCAAAGTCTCGAAGAGTCTCTTTGCCAAATGCGAGAT
 GAGAGATGCTAAATGTGGAAGAAATCCAGTGTCAAGGAGGTGCCAGCGGGCACTCATTTGGTACCAATGCCGTTTC
 CATAGAAACAAACATCCCTCTGCAGCAAGGAGGCGGATTTCTGTGCCGGGGGACCCACGCTGACTTGGCGATGA
 CATGCCGGACCCAGGGCTTGTGCTTGCAGGCACAAAGTGTGCAGATGGAAGAAATCTGCCATGAATCTCAATGTCA
 AAATATTAGTGTCTTTGGGGTTTCAAGTGTGCAATGCAAGTGCACGCGAGAGGGGTGTGCACAAACAGGAAGA
 CTGCCACTGCGAGGCCACTCGGCACTCCCTCTGTGACAAAGTTTGGCTTTGGAGGAAGACACAGACAGCGGCC
 CATCCGGCAGCAGCAAGCAAGGCAAGGAGCTGCAGAGTCCAAAGGAGCGCGGCCAGGCGCAGGAGCCCGTGGG
 ATGCGAGGAGATGCGCTCTA CTGCTCTACTGACATCATCTGAGCCCTCCCATGACATGGAGACCGTGACCAAGT
 TCGCTCGAGAGAGGCTCAGCGCTCCCAAGGCTCTGTGACTGGCAGCATGACTCTGTGGCTTTGCGCATGCTT
 TCCATGACACAGACACACAGTTCTCGGGCTCAGGAGGGGGAAGTCAGGCTACAGGCAAGCTGTCAGAGAA
 CAGTGCAGGAGGCGCAGCGACTTCCTGGTGTAGCTTCTGCTAAGAAATGGACATGCTTCACTGCTGCTCCTGAG
 AGAGTACAGCTTACCATCTGCGAGGCCCCAGCCCTGCAGCAAGGAGGAAGAGGACTCAAAGTGTGGCCCTTTC
 ACTGAGCCCTGCAGCAGTGGGGGAGAAAGCAAGGGTTGGGCCAGTGTCCCTTTCCCCAGTGACACCTCAGCCT
 TGGCAGCCCTGATGACTGGTCTCTGCTGCAACTTAATGCTCTGATATGGCTTTTAGCAATTTATATGAAAAAT
 AGCAGGGTTTGTGTTTAAATTTATCAGAGACCTGCCACCACTTCCATCTCATCAAGCAAACTGAATGGCAA
 TGAACCAACTGGAGAAGAGGTTAGGAGAAAGGGCGGTGAATCTTGGCTCTTGTGTCATGCGGTGACCGAC
 AGTACTCAGGTTTGGGGTTTGCAGAAAGCCAGGGAACCCAGACAGATCACAACCTTCATTAAACAAGTAAGAA
 GTTTAAAGAGTGAACCAATGTAAAGACCTAATCCATCCCCCGTGGCCATTACTGCATAAATAGAGTGCATTT
 GAAAT

1007036-10401

FIGURE 30

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49624

><subunit 1 of 1, 735 aa, 1 stop

><MW: 80177, pI: 7.08, NX(S/T): 5

MAARPLPVSPARALLLALAGALLAPCEARGVSLWNQGRADEVVSASVRSGLWIPVKSFDSK
NHPEVLNIRLQRESKELIINLERNEGLIASSFTETHYLQDGTDVSLARNYTGHCYYHGHVRG
YSDSAVSLSTCSGLRGLIVFENESYVLEPMKSATNRYKLFPKKLKSVRGSCGSHHNTPNLA
AKNVFPPPSQTWARRHKRETLKATKYVELVIVADNREFQRQGDLEKVKQRLIETIANHVDFK
YRPLNIRIVLVGVEVWNDMDKCSVSQDPFTSLHEFLDWRKMKLLPRKSHDNAQLVSGVYFQG
TTIGMAPIMSMCTADQSGGI VMDHSDNPLGAAVTLAHELGHNFNMNHD TLDRCSCQMAVEK
GGCIMNASTGYFPFPMVFSSCSRKDLETSLKGMGVCLFNLPEVRESFGGQKCGNRFVEEGEE
CDCGEPEECMNRCNATTC TLKPDAVCAHGLCCEDCQLKPAGTACRDS SNSCDLPEFCTGAS
PHCPANVYLHDGHSQCQDVG CYNGICQTHEQQCVTLWGP GAKPAPGICFERVNSAGDPYGN
CGKVS KSSFAKCEMRDAKCGKIQCQGGASRPVIGTNAVSIETNIPLQQGGRI LCRGTHVYLG
DDMPDPGLVLGATKCADGKICLN RQCQNI SVFGVHECAMQCHGRGVCNNRKNCHCEAHWAPP
FCDKFGFGSTDSGP IRQAEARQEAAESNRERGGQGEPEVGSQEHASTASLT LI

Signal peptide:

amino acids 1-28

TCCCAAGGCTTCTTGGATGGCAGATGATTNTGGGGTTTTGCATTGTTTCCCTGACAACGAAA
ACAAAACAGTTTTTGGGGGTTT CAGGAGGGGAANTCCAGCCTACCCAGGAAGTTTGAGAAAACA
GTGCAAGGAAGGGCAGGANTTCTCGTTGAGNTTTTTGNTAAACATGGACATGNTTCAGTG
CTGCTCNTGAGAGAGTAGCAGGTTACCACTTTTGGCAGGCCCCAGCCCTGCAGCAGGAGGGA
AGAGGACTCAAAAGTTTGGCCTTTCACTGAGCCTCCACAGCAGTGGGGGAGAAAGCAAGGGTT
GGCCCCAGTGTCCCCTTTCCCCAGTGCACACCTCAGCCTTTGGCAGCCCTGATAACTGGTNTNT
GGCTGCAANTTAATGCTNTGATATGCTTTTAGCATTTATTATATGAAAATAGCAGGGTTTT
AGTTTTTAATTTATCAGAGACCCCTGCCACCCATTTCATNTCCATCCAAG

FIGURE 32

CATCCTGCAACATGGTGAAACCACGCCTGGCTAATTTTGTGTATTTTGGTAGAGATGGGA
TTTCACCGTGTAGCCAGGATGTCTCAATCTGACCTCATGATCTGCCCGCCTCGGCCCTCC
AAAGTGCTGGGATTACAGGCGAGTGCAACCACACCCGGCCACAACTTTTAAAGAAGTTAAT
GAAACCATACCTTTTACATTTTAAATGACAGGAAAAATGCTCACAATAATTTGTTAACCCAAAA
TTCTGGATACAAAAGTACAATCTTTACTGTGTAATACATGTATATGTACTATATGAAAATA
TACCAATATCAATAACTTATCTCTGGGTAAAAACCTCTTCTCATACCCTGTGCTAACAA
CTTTTAAACAAAAATTTGCATCACTTTTAAAGAATCAAGAAAAATTTCTGAAGTTCATATGGG
ACAGAAAAAAAACCAAGGGAAAAATCACGCCACTTGGGAAAAAAGATTGAAATCTGCCT
TTTTATAGATTTGTAATTAATAAGGTCCAGGCTTTCTAAGCACTTAAATGTTTTGTTTCGA
AACAAAGTACTTGTCTGGATGTAGGAGGAAAGGGAGTGATGTCACTGCCATTATGATGCCCC
TTGAATATAAGACCCCTACTTGCTATCTCCCTGCACCAGCCAGGAGCCACCCATCTCCAGC
ACACTGAGCAGCAAGCTGGACACACGGCACACTGATCCAAATGGGTAAGGGGATGGTGGCGA
TGCTCATTCTGGGTCTGCTACTTCTGGCGCTGCTCCTACCCGTGCAGGTTTCTTCATTGT
CCTTTAACAGTATGCCGGAAGCTACTGCAGCCGAAACCACAAAGCCCTCCACAGTGCCT
ACAGCCTACAGCCGCTCTCCTTGTGGTCTTGCTTGCCCTTCTACATCTCTACCATTAAAGAGG
CAGGTCAAGAAACAGCTACAGTTCTCCAACCCATACACTAAAACCGAATCCAAATGGTGCCT
AGAAGTTCAATGTGGCAAGGAAAAAACAGGTCTTCATCAAATCTACTAATTTCACTCCTT
ATTAACAGAGAAACGCTTGAGAGTCTCAAACCTGGAAGTGTAAAGAGCATCTGAAGGATTT
GACTAGATGATAAATGCCTGTACTCCAGTACTTTGGGAGGCCCTAGGCCGCGGATCACCTG
AGGTCAGGAGTTTGAGACTAACCTGGCCAAAATGGTGAAACCCCATCTGTACTAAAAATACA
AATATTGACTGGGCGTGGTGGTGAAGTGCCTGTGATCCAGCTACTCAGGTGGCTGAAGCAGG
ACAATCACTTGAACTCAGGAGGCAGAGGTGCAAGTGAGCTGAGATCGCGCTACTGCACTCTA
GCCTAGCCTGGGCAACAGAGTGAGACTTCGTCTCAAAAAAAAAAAGCCAAGTGCAAGTGGCT
CACGCCTGTAATCCCGGCACTTTGGGAGGCCGAGGTGGGCGGATCACGAGGTCAGGAGATCA
AGACCATCCTGGCTAATACAGTGAAACCTGTCTCTACTAAAAATACAAAAATAGCCGGG
GATGGTGGCAGGCACCTGGAGTCCAGCTACTCGGAGGCTGAGGCAGGAGATAGCGTGAA
CTCAGGAGGCGGAGCTGCAAGTGAGCCGAGATTGCGCTACTGCACTCCAGCCTGGGCGACAG
CGCGAGACTCCGTCTCAAAAAAAAAAAAAAAAAAAAAA

FIGURE 33

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48309

><subunit 1 of 1, 67 aa, 1 stop

><MW: 6981, pI: 7.47, NX(S/T): 0

MGKGMVAMLILGLLLALLLPVQVSSFVPLTSMPEATAAETTKPSNSALQPTAGLLVVLLAL
LHLYH

Signal peptide:

amino acids 15-27

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FIGURE 34

CCCGCGCGAGAGCGCGCCGACGCCCGCGCGGATGCCGCGCGCCAGGACGCCTCTCCCGTGTGCGGCCGG
CGGCGGCCCTGACTCGCTGCTGCTGCTGCTGCTGGCCATGGCGCGCGCGGGCGCTGGGGCGCCCGGGCCAGG
AGGCGGCGCGCGCGCGCGGAGCGGGCCCCCGCGGACAGCGCGAGGACGGACAGGACCCGACAGCAGCACC
TGTACACGCGCGACATGTTACGCGACGGGATCCAGAGCGCGCGCACTTCGCTCATGTTCTTCGCGCCCTGGTGTG
GACACTCGCAGCGGCTGCAGCGCACTTGGAAATGACCTGGGAGACAATAACAACAGCATGGAGATGCCAAAGTCT
ATGTGGCTAAAGTGGACTGCAGCGGCCCACTCCGACGTGTGCTCCGCCCCAGGGGTGCGAGGATACCCCACTTAA
AGCTTTTCAAGCGAGGCCAAGACCTGTGAAGTACAGGGTCTCGGGACTTCCAGACACTGGAAAACTGGATGC
TGCAGACACTGAACCGAGGAGCCAGTGCACCGAGGCGGAAAGCCCGCCAGTGCCTCCGAGCTCAAGCAAG
GGCTGTATGAGCTCTCAGCAAGCAACTTTGAGCTGCGAGTGTGCACAGGCGACCACTTTATCAAGTCTTCTTCGCT
CGTGGTGTGGTCACTGCAAGGCCCTGGCTCCAACTGGGAGCAGCTGGCTCGGGCTTGAACATTCGAAACTG
TCAAGATTGGCAAGTGTGATTGTACACAGCACTATGAACCTCTGCTCCGGAAACAGGTTCTGGCTATCCCACT
TCTCTCGTTCGAGATGGGAAAAAGGTGGATCAGTACAAGGGAAAGCGGATTTGGAGTCACTGAGGGAGTACG
TGGAGTCCGAGCTGCAGCGCACAGAGACTGGAGCGACGAGACCGTCAAGCCCTCAGAGGCCCGGTGCTGGCAG
CTGAGCCCGAGGCTGACAAGGGCACTGTGTTGGCACTCACTGAAAATAACTTCGATGACACCATTCGAGAAGGAA
TAACCTTCATCAAGTTTATGTCTCCATGGTGTGGTCATTGAAGACTCTGGCTCCTACTTTGGGAGGAACCTCTCTA
AAAAGGAATTCCTGGTCTGGCGGGGGTCAAGATCGCGGAAGTAGACTGCACCTGCTGAACGGAATATCTGCAGCA
AGTATTCGGTACGAGGCTACCCCACTGTTATGCTTTCCGAGGAGGGAAGAAAGTCAGTGAGCACTGAGGAGCA
GAGACCTTGACTCGTTACACCGCTTTGTCTGAGCCAAGCGAAAGACGAACCTTAGGAACACAGTTGGAGGTAC
CTCTCTGCGCCAGCTCCCGCACCTTGCCTTAGGAGTTTCACTCCACAGAGGCCACTGGGTTCCAGTGGTGGCT
GTTTCAGAAAGCAGAACATATAAGCGTGAGGTATCTCTTTGTGTGTGTGTTTCCAAAGCCAACACACTCTACAG
ATTCTTTATTAAGTTAAGTTCTCTAAGTAAATGTAACTCATGGTCACTGTGTAAACATTTTTCAGTGGCGATA
TATCCCTTTGACCTTCTCTGTGATGAATTTACATGGTTTCCCTTGAGACTAAAAATAGCGTTGAGGGAATGAAA
TTGCTGGACTATTGTGGCTCTCGAGTTGAGTGATTGTTGGTGAAGAAAGCACATCCAAAGCATAGTTTACCTGC
CCACGAGTTCTGGAAGGTGGCTTGTGGCAGTATTGACGTTCCCTCGATCTTAAGGTCAAGTTGACTCAANTAC
TGTGTTGGTCCGTAGCATGGAGCAGATTGAAATGCAAAACCACACCTCTGGAAGATACCTTCAAGGCCGCTGC
TGGAGCTTCTGTTGCTGTGAATACTTCTCAGTGTGAGAGGTAGCCGTGAAGACAGCGTTACTTCTGACC
GTGCTGAGTAAGAGAATGCTGATGCCATAACTTTATGTGTGCGATCTGTGCAAAATCACTTACTGTTCAGGGAT
CCTTCTGTTTCTCAGCGGGTGAACATGCTTTAGTTCCCTCATGTTAACACGAAGCCAGAGCCCACTGAACGT
TGGATGCTTCTCTAGAAAGGTTAGGCATGGAATAATCCAGAGGCTCATCTCAGTATCTTATTAACCTATTGA
AAGATTCCAGTTGATTTTGTCACTCGGGGTGACAAGACCAGACAGCGCTTCCAGGCCCTGGGTATCCAGGGAGC
TCTGCGAGCCCTGTAAGGGCCCTTAACTAGAGTTCTAGACTTTCTGATTCTGTTTCTCAGTAGTCCCTTTAGAGG
CTTGCTATACTGGGTGCTGCTTCAAGGAGGTGACCTTCTAATGTATGAAGAATGGGATGCATTGTATCTCAAGAC
CAAAGACAGATGTCAGTGGGCTGCTCTGCGCCCTGCTGTGCAAGGCTGTGGCAGCTGTGATGCGCCCTCTA
ACTCATGCTGCTGTGATTAACCACTCTATCTCCCTTGGGAATAGCACATACAGGCTTAAGCTCTAAGATA
GATAGTGTGTTGCTTTTACCATCGAGTACTTCCCATATAAACCACTTTTCTGATCCCAACACTCTTACCCCACT
CCCATACGCAAGGATGAGTACTTGGCCCAAAGTAACCTGGTGGTAGGAATCTTAGAAACAAAGACCACTTATA
CTGTCTGTCTGAGGCAAGAATACAGCAGCATCTCGACCAGCCTCTGCTTAAAGGAAATCTTTATTAAATCAG
TATGGTTCACAGATAATCTTTTAAAAAAACCCCACTCTAGAGAAGCACACTGTCAAGAGTCTGTGATCA
CACACTTCAGCTTTGCTACAGAGCTCTGTATTCAGAAAGAAATCAAAGTGGTACAAATTTGTGTTTACACTAT
GATACTTTCTAAATAACTCTTTTTTTTTAA

FIGURE 35

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA46776

><subunit 1 of 1, 432 aa, 1 stop

><MW: 47629, pI: 5.90, NX(S/T): 0

MPARPGRLLPLLARPAALTALLLLLLGHGGGGRWGARAQEAAAAAADGPPAADGEDGQDPHS
KHLTYADMFTTHGIQSAAHFVMFFAPWCGHCQRLQPTWNDLGDKYNSMEDAKVYVAKVDCTAH
SDVCSAQGVRGYPTLKLFKPGQEAVKYQGPRDFQTLLENWMLQTLNEEPVTPEPEVEPPSAPE
LKQGLYELSSASFELHVAQQGDHFIKFFAPWCGHCKALAPTWEQLALGLEHSETVKIGKVDCT
QHYELCSGNQVRGYPTLLWFRDGKKVDQYKGRDLESLEYYVESQLQRTETGATETVTPSEA
PVLAAEPEADKGTVLALTENNFDDTIAEGITFIKFYAPWCGHCKTLAPTWEELSKKEFPGLA
GVKIAEVDCTAERNICSKYSVRGYPTLLLFRGGKKVSEHSGGRDLDLSLHRFVLSQAKDEL

Signal sequence:

amino acids 1-32

FIGURE 36

CTTTTCTGAGGAACACAGCAATGAATGGCTTTGCATCCTTGCTTCGAAGAAACCAATTTAT
CCTCCTGGTACTATTTCTTTTGCAAATTCAGAGTCTGGGTCTGGATATTGATAGCCGTCCTA
CCGCTGAAGTCTGTGCCACACACAATTCACCAGGACCCAAAGGAGATGATGGTGAAAAA
GGAGATCCAGGAGAAGAGGGAAAGCATGGCAAAGTGGGACGCATGGGGCCGAAGGAATTAA
AGGAGAACTGGGTGATATGGGAGATCAGGGCAATATTGGCAAGACTGGGCCCATTTGGGAAGA
AGGGTGACAAAGGGGAAAAAGGTTTGCTTGGAATACCTGGAGAAAAAGGCAAAGCAGGTACT
GTCTGTGATTGTGGAAGATACCGGAAATTTGTTGGACAACCTGGATATTAGTATTGCTCGGCT
CAAGACATCTATGAAGTTTGTCAAGAATGTGATAGCAGGGATTAGGGAACTGAAGAGAAAT
TCTACTACATCGTGCAGGAAGAGAAGAACTACAGGGAATCCCTAACCCTGCAGGATTCGG
GGTGAATGCTAGCCATGCCAAGGATGAAGCTGCCAACACACTCATCGCTGACTATGTTGC
CAAGAGTGGCTTCTTTGGGTGTTTCATTGGCGTGAATGACCTTGAAAGGGAGGACAGTACA
TGTCACAGACAACACTCCACTGCAGAACTATAGCAACTGGAATGAGGGGGAACCCAGCGAC
CCCTATGGTCATGAGGACTGTGTGGAGATGCTGAGCTCTGGCAGATGGAATGACACAGAGTG
CCATCTTACCATGTACTTTGTCTGTGAGTTTCATCAAGAAGAAAAAGTAACTTCCCTCATCCT
ACGTATTTGCTATTTTCTGTGACCGTCATTACAGTTATTGTTATCCATCCTTTTTTTCCTG
ATTGTACTACATTGATCTGAGTCAACATAGCTAGAAAATGCTAAACTGAGGTATGGAGCCT
CCATCATCAAAAAAAAAAAAAAA

FIGURE 37

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50980
><subunit 1 of 1, 277 aa, 1 stop
><MW: 30645, pI: 7.47, NX(S/T): 2
MNGFASLLRRNQFILLVFLLLQIQSLGLDIDSRPTAEVCATHTTISPGPKGDDGEKGDPEEG
KHGKVGMRMGPKGIKGELGDMGDQGNIGKTGPICKKGDKGEKGLLGIPGEKKGAGTVCDGGRY
RKFGVQLDISIARLKTSMKFVKNVIAGIRETEEFYFYIVQEEKNYRESLTHCRIRGGMLAMP
KDEAANTLIADYVAKSGFFRVFIGVNDLEREGQYMSTDNTPLQNYSNWNEGEPSDPYGHEDC
VEMLSSGRWNDECHLTMYFVCFIKKKK
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Signal peptide:

amino acids 1-25

FIGURE 38

GGTTCTATCGATTGCAATTCGGCCACACTGGCCGGATCCTCTAGAGATCCCTCGACCTCGAC
CCACGCGTCCGCTGCTCTCCGCCCGTGTGGAGTGGTGGGGGCTGGGTGGGAATGGGCGTGT
GCCAGCGCAGCGCGCTCCCTGGAAGGAGAAGTCTCAGCTAGAACGAGCGGCCCTAGGTTT
CGGAAGGGAGGATCAGGGATGTTTCCGAGCGGCTGGAAACGAGACGGTGCCGATAGAGGAAG
GGGCTCCATGGCTGCCCTCCTGCTGCTGCCCTGCTGCTGTTGCTACCGCTGCTGCTGCTGA
AGCTACACCTCTGGCCGCGAGTTGCGCTGGCTTCCGGCGGACTTGGCCTTTGCGGTGCGAGCT
CTGTGCTGCAAAAGGGCTCTTCGAGCTCGCGCCTGGCCGCGGCTGCCGCCGACCCGGAAAG
TCCCCAGGGGGGCTGCAGGCTTGGCTTGGCGCCTCGCGGAACCTGGCCCAGCAGCGCGCCGCGC
ACACCTTTCTCAITCACGGCTCGCGCGCTTTAGCTACTCAGAGGCGGAGCGCGAGAGTAAC
AGGGCTGCACGCGCCTTCTCAGTGCGCTAGGCTGGGACTGGGGACCCGACGGCGCGCAG
CGGCGAGGGGAGCGCTGGAGAAGGCGAGCGGGCAGCGCCGGAGCCGGAGATCAGCGCGCCG
GAAGCGCGCGGAGTTTCCGCGAGGGGACGGTGCCGCCAGAGGTGGAGGAGCCGCCGCCCT
CTGTACCTGGAGCAACTGTGGCGTGCTCCTCCCCGCTGGCCCAGAGTTTCTGTGGCTCTG
GTTCCGGCTGGCCAAAGCCCGCTGCGCACTGCCTTTGTGCCACCGCCTTGCGCCGGGGCC
CCCTGCTGCATGCTCCCGAGCTCGCGCGCGCGCGCTGGTGCTGGCGCGAGAGTTTCTG
GAGTCCCTGGAGCCCGGACCTGCCGCCCTTGAGAGCCATGGGGCTCCACCTGTGGGCTGCAGG
CCAGGAACCACTCTGCTGGAATTAGCGATTTGTGGCTGAAGTGTCCGCTGAAGTGGATG
GGCCAGTGCCAGGATACTCTCTTCCCCCAGAGCATAACAGACAGCTGCCCTGTACATCTT
ACCTCTGGCACCACGGGCCTCCCCAAGGCTGCTCGGATCAGTCATCTGAAGATCCTGCAATG
CCAGGCTTCTATCAGCTGTGTGGTGTCACAGGAAGATGTGATCTACCTCGCCCTCCAC
TCTACCACATGTCGGTTCCTGTCTGGGCATCTGGGCTGCATGGGCATTGGGGCCACAGTG
GTGCTGAAATCCAAGTTCTCGGCTGGTCAGTTCTGGGAAGATTGCCAGCAGCACAGGTTGAC
GGTGTTCAGTACATTGGGGAGCTGTGCCGATACCTTGTCAACAGCCCGCAGCAAGGCAG
AACGTGGCCATAAGTCCGGCTGGCAGTGGGCAGCGGGCTGCGCCAGATACCTGGGAGCGT
TTTGTGCGGCGCTTCGGGCCCTTGCAAGTGCTGGAGACATATGGACTGACAGAGGGCAAGT
GGCCACCATCAACTACACAGGACAGCGGGGCGCTGTGGGGCGTGCTTCTGGCTTTACAAGC
ATATCTTCCCTTCTCCTTGATTGCTATGATGTACCAACAGGAGAGCCAAATTCGGGACCCC
CAGGGGCACTGTATGGCCACATCTCCAGGTGAGCCAGGGCTGCTGGTGGCCCCGGTAAGCCA
GCAGTCCCCATTCTGGGCTATGCTGGCGGGCCAGAGCTGGCCCAGGGGAAGTTGCTAAAGG
ATGTCTTCCGGCTGGGATGTTTTCTTCAACACTGGGACCTGCTGGTCTGCGATGACCAA
GGTTTTCTCCGCTTCCATGATCGTACTGGAGACACCTTCAGGTGGAAGGGGGAGAATGTGGC
CACAAACGAGGTGGCAGAGGTCTTCGAGGCCCTAGATTTTCTTCAGGAGGTGAACGTCTATG
GAGTCACTGTGCCAGGGCATGAAGGCAGGGCTGGAATGGCAGCCCTAGTTCTGCGTCCCCC
CACGCTTTGGACCTTATGCAGCTCTACACCCACGTGTCTGAGAAGTTGCCACCTTATGCCCG
GCCCGGATTCCTCAGGCTCCAGGAGTCTTTGGCCACCACAGAGACCTTCAAACAGCAGAAAG
TTCGGATGGCAAAATGAGGGCTTCGACCCAGCACCCGTCTGACCCCACTGACCTTCTGGAC
CAGGCTGTAGGTGCCCTACCTGCCCTCACAACCTGCCCGGTACAGCGCCCTCTTGGCAGGAAA
CCTTCGAATCTGAAGACTCCACACCTGAGGCACCTGAGAGAGGAACTCTGTGGGGTGGGGG
CCGTTGCAGGTGTACTGGGCTGTGAGGATCTTTCTATACCAGAACTGCGGCTCACTATTTT
GTAATAAATGTGGCTGGAGCTGATCCAGCTGTCTCTGACCTAAAAAAAAAAAAAAAAAAAA
AAAAAAGGGCGGCGCAGTCTAGAGTCAGCTGAGTAGGATAACAGGGTAATAAGC
TTGGCCGCCATGGCCCACTTGTTTATTGCAG

FIGURE 39

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50913
><subunit 1 of 1, 730 aa, 1 stop
><MW: 78644, pI: 7.65, NX(S/T): 2
MGVCQRTRAPWKEKSQLEAALGFRKGGSGMFASGWNQTVPIEEAGSMAALLLLPLLLLLPL
LLLKLHLWPQLRWLPADLAFVAVRALCCKRALRARALAAAAADPEGPEGGCSLAWRLAELAQQ
RAAHTFLIHGSRFFSYSEAERESNRAARAFRLALGWDWGPDGGDSGEGSAGEGERAAPGAGD
AAAGSGAEFAGGDGAARGGGAAAPLSPGATVALLLPAGPEFLWLWFGLAKAGLRTAFVPTAL
RRGPLLHCLRSCGARALVLAPEFLESLEPDLPALRAMGLHLWAAGPGTHPAGISDLLAEVSA
EVDGVPVPGYLSPPQSITDTCLYIFTSGTTGLPKAARISHLKILQCQGFYQLCGVHQEDVIYL
ALPLYHMSGSLLGIVGCMGIGATVVVLKSKFSAGQFWEDCQQHRVTVFQYIGELCRYLVNQPP
SKAERGHKVRILAVGSGLRPDTWERFVRRFGPLQVLETYGLTEGNVATINYTGQRGAVGRASW
LYKHIFPFSLIRYDVTTGEPIRDPOGHCMATSPGEPGLLVAPVSQQSPFLGYAGGPPELAQ GK
LLKDVFVRPGDVFFNTGDLLVCDQGFRLRFHDRTGDTFRWKGENVATTEVAEVFEALDFLQEV
NVYGVTVPGHEGRAGMAALVLRPPHALDLMQLYTHVSENLPYARPRFLRLQESLATTETFK
QQKVRMANEGFDPSTLSDPLYVLDQAVGAYLPLTTARYSALLAGNLRI

Type II transmembrane domain:

amino acids 45-65

Other transmembrane domain:

amino acids 379-398

cAMP- and cGMP-dependent protein kinase phosphorylation site
starting at amino acid 136

CUB domain protein motif

amino acids 254-261

putative AMP-binding domain signature

amino acids 332-343

N-glycosylation sites

amino acids 37-40 and 483-486

FIGURE 40

CCTGTGTTAAGCTGAGGTTTCCCCTAGATCTCGTATATCCCCAACACATACCTCCACGCACAC
CACATCCCCAAGAACCTCGAGCTCACACCAACAGACACACGCGCGCATACACACTCGCTCTC
GCTTGTCCATCTCCCTCCCGGGGAGCCGCGCGCGCTCCCCACCTTTGCCGCACACTCCGCG
GAGCCGAGCCCGCAGCGCTCCAGGATTCTGCGGCTCGGAACTCGGATTGCACTCTGGAACCC
CCATGGTGGTTTTTTAAACACTTCTTTTCTCTCTCTCTCGTTTGGATTGCAACCGTTTCCA
TCTGGGGCTAGAGGAGCAAGGCAGCAGCCTTCCCAGCCAGCCCTTGTGGGCTTGCCATCGT
CCATCTGGCTTATAAAAGTTTGTGAGCGCAGTCCAGAGGCTCGCGTGTCTGTCCTCCCTCGG
CTGGCAGAGGGGGTGACGCTGGGCAGCGGCAGGAGCGCGCCGCTGCTCTGCGCGGCTTT
CGGCTTAGGGGGCAAGGTGAAGAGCGCACCGGCCGTGGGGTTTACCAGCTGGATTGTGTATG
TGTGACCATTGCTCTCTGGATCGGGGCTGTGATTCTTCCCTCTTGGGGCTGCTGCTCTCCC
TCCCCGCGGGGCGGATGTGAAGGCTCGGAGCTGCGGAGAGGTCGCCAGGCGTACGGTGCC
AAGGGATTACGCTTGGCGGACATCCCCCTACCAGGAGATCGCAGGGGAACACTTAAGAATCTG
TCCTCAGGAATATACATGCTGCACCACAGAAATGGAAGACAAGTTAAGCCAACAAAGCAAA
TCGAATTTGAAAACCTTGTGGAAGAGACAAGCATTTTGTGCGCACCCTTTGTGTCCAGG
CATAAGAAATTTGACGAATTTTCCGAGAGCTCCTGGAGAACTCGAAGAAAGTCACTAAATGA
TATGTTTGTACGGACCTATGGCATGCTGTACATGCAGAAATCAGAAGTCTTCCAGGACCTCT
TCACAGAGCTGAAAGAGTACTACACTGGGGCTAATGTGAACTCGAGGAAATGCTCAATGAC
TTTTGGGCTCGGCTCTTGGAACGGATGTTTCAGCTGATAAAACCTCAGTATCACTTCAGTGA
AGACTACCTGGAATGTGTGAGCAAATACACTGACCAGCTCAAGCCATTGGAGACGTGCCCC
GGAAACTGAAGATTTCAGGTTACCCGCGCTTTCATTGCTGCCAGGACCTTTGTCCAGGGGTG
ACTGTGGGCAGAGAAGTTGCAAACCGAGTTTCCAAGGTCAGCCCCAACCCAGGGTGTATCCG
TGCCCTCATGAAGATGCTGTACTGCCCATCTGTGCGGGGCTTCCCCTGTGAGGCCCTGCA
ACAACACTGTCTCAACGTCATGAAGGGCTGCTTGGCAAATCAGGCTGACCTCGACACAGAG
TGGAACTCTGTTTATAGATGCAATGCTCTTGGTGGCAGAGCGCATGGGAGGGGCATTCAACAT
TGAGTCGGTCATGGACCCGATAGATGTCAAGATTTCTGAAGCCATTATGAACATGCAAGAAA
ACAGCATGCAGTGTCTGCAAAAGTCTTTTCAGGGATGTGGTCAGCCCCAAACCTGCTCCAGCC
CTCAGATCTGCCCCCTCAGCTCCTGAAAATTTTAATACACGTTTCAGGCCCTACAATCCTGA
GGAAAGACCAACAACCTGCTGCAGGCACAAGCTTGGACCGGCTGGTCACAGACATAAAAGAGA
AATTGAAGCTCTCTAAAAAGGTCTGGTCAGCATTACCCTACACTATCTGCAAGGACGAGAGC
GTGACAGCGGGCACGTTCAAACGAGGAGGAATGCTGGAACGGGCACAGCAAAGCCAGATACTT
GCCTGAGATCATGAATGTGGGCTCACCAACCAGATCAACAATCCCGAGGTGGATGTGGACA
TCACTCGGCCTGACACTTTTCATCAGACAGCAGATTATGGCTCTCCGTGTGATGACCAACAAA
CTAAAAAACGCCTACAATGGCAATGATGTCAATTTCCAGGACACAAGTGATGAATCCAGTGG
CTCAGGGAGTGGCAGTGGGTGCATGAGATGACGTGTGTCCCACGGAGTTTGAAGTTTGTACCA
CAGAGGCCCCCGCAGTGGATCCCGACCGGAGAGAGGTGGACTCTTCTGCAGCCAGCGTGGC
CACTCCCTGCTCTCTGGTCTCTCACTGCAATGTCTCTGGCACTGCAGAGACTGTGCAGATA
ATCTTGGGTTTTTGGTCAGATGAAACTGCATTTTAGCTATCTGAATGGCCAACCTCACTTCTT
TCTTACACTCTTGGACAATGGACCATGCCACAAAACTTACCGTTTTCTATGAGAAGAGAG
CAGTAATGCAATCTGCTCCTCTTTTGTGTTTTCCAAAGAGTACCGGTGCGCAGACTGAACTG
CTCTCTCTTCTCTCAGTATCTGTGGGACCTGTTTATTCTAGAGAGAATTCTTACTCAA
ATTTTTCTACCAGGAGATTTCTTACCTCTATTGCTTTTATGCTGCAGAAGTAAAGGAAT
CTCAGTGTGAGGGTTTTTTTTTTCTCATTTAAAT

FIGURE 41

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50914

><subunit 1 of 1, 555 aa, 1 stop

><MW: 62736, pI: 5.36, NX(S/T): 0

MPSWIGAVILPLLGLLLSLPAGADV KARSCEVRQAYGAKGFS LADIPYQEIAGEHLRICQ
EYTCCTTEMEDKLSQQSKLEFENLVEETSHFVRTTFVSRHKKFDEFFRELL ENAEKSLNDMF
VRTYGLMYMQNSEV FQDLFTELKRYTGGNVNLEEMLNDFWARLLERM FQLINPQYHFS EDY
LECVSKYTDQLKPFQDVP RKLKIQVTRAFIAARTFVQGLTVGREVANRVSKVSPTPGCIRAL
MKMLYCPYCRGLPTVRPCNNYCLNVMKGCLANQADLDTEWNLFIDAMLLVAERLEGPFNIES
VMDPIDVKISEAIMNQENSMQVSAKV FQCGQPKPAPALRSARSAPENFNTRFRPYNPEER
PTTAAGTSLDRLVTDIKEKLKLSKKVWSALPYTICKDESVTAGTSNEEECWNGH SKARYLPE
IMNDGLTNQINNPEVDVDITRPDTFIRQQIMALRVMTNKLKNAYNGNDVNFQDTSDESSGSG
SGSGCMDDVCPTEFEFVTTEAPAVDPDRREVDSSAAQRGHSLLSWSLTCIVLALQRLCR

Signal peptide:

amino acids 1-23

FIGURE 42A

CGGACGCGTGGGCGGACGCGTGGGCGAAAGAACTCGGAGTGCCAAAGCTAAATAAGTTAGCTGAGAAAAACGCA CG
CAGTTTGCAGCGCCTCGCGCGGGTGCGCCAACTACGCAAAAGACCAAGCGGGCTCCGCGGAGACCGGCGCGGGGC
TAGGGACCCGGCTTTGGCCTTCAGGCTCCCTAGCAGCGGGGAAAAGGAATTGCTGCCCGGAGTTTCTGCGGGAGGT
GGAGGGAGATCAGGAAACGGCTTCTTCCTCACTTCGCGCGCTGGTGAGTGTGCGGGAGATGGCGAAACGCGCTTAGG
AAAGGACTGGGGAAATAGCCCTGGGAAAGTGAGAAAGTGATCAGGAGGCGCGTCCACTACGGCAGTTTATCTG
TCTGATCAGAGCCAGACGCGAGCGCTCCACTTCGCGATTCTTTCAGGTGTGGGACCCGAGGACAGCGGCGCA
TCCGCGCGCCCTCGTACCAGCACTCCAGGAGAGTCAGCCTCGCTCCCCAACCTCGAGGGCGCTCTGGCCACGA
AAAGTTCTGTCCACTGTGATTCTCAATTCTTGTCTGGTTTTCCTCCAGAGAACTTTGGGTGGAGATATTA
ACTTTTTCCTTTTTTTTTCCTTGGTGAAGCTGCTCAGGGAGGGGGAGGAGGAGAGAAAGTGAATGTGC
TGGAGAAGAGCGAGCCCTCCTTGTTCCTCCGAGTCCCATCCATTAGCCATCACTTCGGAAGATTAAAGTTGT
CGGACATGTTGACAGCTGAGAGGAGAGGAGGATTTCTTCCAGGTGGAGAGTCTTCAACGCTCTGTGGGTGCATG
TGTGCGCCCGCAGCGGCGCGGGGCGCGTGGTTCTCGCGTGGAGTCTCACTGGGACCTGAGTGAATGGCTCCCA
GGGCTGTGCGGGGCATCGCGCTCGCCTTCTCCACAGGCTGTGTCTGTCTGGAAGATGCTAGCAATGGGGG
CGCTGGCAGGATTCTGGATCTCTGCCTCTCACTTATGTGTTACCTGTCTGGGGCCAGGCGCTTAGAAGAGGAGG
AAGAAGGGGCTAGACTCTCAAGCTGGAGAGAACTAGAGCCAGCACAACTCCACCTCCGAGCCCCATCTCA
TTTTTCATCTAGCGGATGATCAGGATTTAGAGATGTGGGTACCACGGATCTGAGATTAAAAACACCTACTCTTG
ACAAGCTCGCTGCGAAGGAGTTAACTGGAGAACTACTATGTCCAGCCTATTGTGACACCATCCGAGAGTCAGT
TTATTACTGGAAGTATCAGATACACCCGGACTTCAACATTTCTATCATAGACCTTACCAACCCCACTGTTTAC
CTCTGGACAATGCCACCTTACCTCAGAACTGAAGGAGGTGGATATTCAACGCATATGCTCGGAAAATGGCACT
TGGGTTTAAACAGAAAAGAATGCATGCCACAGAAAGAGGATTGATACCTTTTGGTTCCCTTTTGGGAAAGTG
GGGATTA CTATACACACTACAAATGTGACAGTCC TGGGATGTGTGGCTATGACTTGTATGAAAACGACAATGCTG
CCTGGGACTATGACAAATGGCATATACTCCACACAGATGTACACTCAGAGAGTACAGCAAACTTAGCTTCCCAT
ACCCCAACAAGCTTATATTTTTATATACTGCCTATCAAGCTGTTCATTCCACACTGCAAGCTCCTGGCAGGTATT
TCGAACACTACCGATCCATTATCAACATAAACAGGAGAAGATATGTCCTTCTGCTTAGATGAAGCAA
TCAACAACGTGACATTGGCTCTAAAGACTTATGGTTTCTATAAACACAGCATATTATTTACTCTTCAGATAATG
GTGGCCAGCCTACGGCAGGAGGGAGTAATGGCCTCTCAGAGGTAGCAAAGGAACATATTGGGAAGGAGGATCC
GGGCTGTAGGCTTTGTGCATAGCCCACTTCTGAAAAACAAGGGAACAGTGTGTAAGGAACCTTGTGCACATCACTG
ACTGTATACCCCACTCTCACTTTCAGCTGGCTGAAGGACAGATTGATGAGGACATTCACTAGATGGCTATGATATCT
GGGAGACCATAAGTGAGGGTCTTCGCTCACCCCGAGTAGATATTTTGTGATAACATTGACCCCTATACACCAAGC
AAAAAATGGCTCCTGGGCAGCAGGCTATGGGATCTGGAACACTGCAATCCAGTCAGCCATCAGAGTGCAGCACTG
GAAATGTCTTACAGGAAATCCTGCTACAGCGACTGGGTCCCCCTCAGTCTTTTCAAGCAACTGGGACCGAACC
GTGGCAACAATGAACGATCACTTGTCACTGGCAAGAGTGTATGGCTTTTCAACATCAGACCGACCCATATGA
GAGGGTGGACATCTTAA CAGGTATCCAGGAATCGTGAAGAAGCTCCTACGGAGGCTCTCACAGTTCAACAAAG
TGCAGTGCCTGTCAGGTATCCCCCAAGACCCAGAAAGTAACCTAGGCTCAATGGAGGGGCTCTGGGACCATG
GTATAAAGAGGAAACCAAGAAAAAGAGCCAGCAAAATCAGGCTGAGAAAAAGCAAAGAAAAAGCAAAAAA
GAAGAAGAAACAGCAGAAAGCAGTCTCAGGTAACCCAGCAAAATTTGGCTCGATAATATTCGCTGGCTAAGCGTCA
GGCTGTGTTTTCATGCTGTGGCCACTCTCAGAGACTTCTGCCACTGGCCGCCACACTGAAACCTGCTCTGCTCAGTG
CCAAGTGCTACTCTTGAAGCCACACTTAGAGAGATGGAGTGTATTCTCTGCTCCTTTAGAAAAAGCTG
GTGAGTCTGAGTTCAGTCTGTGCTTCACTCAACTGACCAAACTGCTTTGAATTATAGGAGGAGAACATA
ACCTACCATCCGCAAGCATGCTAATTGTATGGAAGTTACAGGGTAGCATGATTAAACTACCTTTGATAAATTAC

FIGURE 42B

AGTCAAAGATTGTGTACCTCAAGGCCTTGAAGAATATATTTTCTGGTGAATTTTGTATGTCTGTATATGA
CACTTGGGTTTTTAAATTAATCTATTTTATATATATAAATATATGTTTCTTTCTGTGAAAAGCTGTTTTCT
CACATGTGAACAGCTTGCACCTCATTTTACCATGCGTGAGGGAATGGCAAATAAGAATGTTTGAGCACACTGCC
ACRAATGAATGTAACATTTTTCTAAACACTTTACTAGAAGAACATTTTCAGTATAAAAAACCTAATTTATTTTACA
GAAAAATATTTTGTGTTTTTATAAAAAAGTTATGCAAAATGACTTTTATTTTATTTCCTGCATACCATTTAGAAGA
ATTTTATTTTCATTTTCTCAAATTTATCAAGCACGTAACTATAAATTAATGTAATACTGTGTGAATTCAGACTA
TAAAAAACATCATTCAGAAAACTTTATAATCGTCATTGTTCAATCAAGATTTTGAATGTAATAAGATGAATATAT
ATTACTTGGAAATCAATGTTTGTGCAGAGTTGAGACAACTTTATTGTTTCTATCATAACTATTTATGATATCTT
AATTATTAAATGATTTTACTTTATGGCACTAGAAAAATTTACTGTGGCTTTTCTGATCTAAGCTCTAGCTAAAAAT
GTATCATTTGGTCTAAAAAATAAAAAATCTTTACTAATAGGCAATTGAAGGAATGGTTTGCTAACCAACCAAGTAA
TATAATATGATTTTACAGATAGATGCTTCCCCTGGCTATGACATGGAGAAAGATTTTCCCATATAATAAAGTAA
TATTTATATTAGGTTGGTGCAAACTAGTTGCGGTTTTTCCCATTTAAAGTAATAACCTTACTCTTATACAAAGT
GGACACTGTGGGGAGATACAGAGAAATGGAAGATACGGATCCTGCCTGGATAGGTAACTTGCCTGGAAACCCC
ACATGCAACGTCATGAGGAGAAATTAAGGAGTATTATCAGTAATGAAGTTTATCATGGGTCATCAATGAGCATA
GATTGGTGTTGATCCTGTAGACCTCGGTGTTTTCTTTGAAGTGCCCTCTCCTAATGCAGAGGCCCTGAAGCTTAC
AGTATACACTTGAAAAGTCACAGATAGCTAGAATTATGATCTTTGAAGTTATAACTGTGATCTGAAAATGTGTGT
GGTGGTATGACAGCATACCATTAATACATTACATCACAGCTCAAAGGACTGTGATATAATCCATTTATATCAC
AACTCAAAGGACTGTGATATAATCCATTTATATCACAGCTCACAGTTTCTGAAAAATGTATAAAAAGATCTATAAT
CTAGTACTGAAATTACTAAATTTGGGTAAGATGATTTAAATGATTTAAATTTAACATTTTATTTCTAGAAATATAT
GGCTCCATTTTATTTTATAGTGTAAAGTTGTATTTCCCTAAAGTTTGTGTTTTGTGCGACAGTATCTTTTAAATGAG
TCTTAAAAATAAAGGCATATTGTTTCATGTTTAAA
AAA

42B

FIGURE 43

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48296

><subunit 1 of 1, 515 aa, 1 stop

><MW: 56885, pI: 6.49, NX(S/T): 5

MAPRGCAGHPPPPSPQACVCPGKMLAMGALAGFWILCLLTYGYLSWGQALEEEEEEGALLAQA
GEKLEPSTTSTSQPHLIFILADDQGFRDVGYHGSEIKTPTLDKLAATEGVKLENYYVQPICTP
SRSQFITGKYQIHTGLQHSIIIRPTQPNCLPLDNATLPQKLKEVGYSTHMGVKGWHLGPNRKEC
MPTRRGFDTFFGSLLGSGDYIYTHYKCDSPGMCYDLYENDNAAWDYDNGIYSTQMYTQRVQQ
ILASHNPTKPIFLYTAYQAVHSPLQAPGRYFEHYRSIININRRRYAAMLSCLEAINNVTLA
LKTYGFYNNHSIIYSSDNGGQPTAGGSNWPLRGSKGTWEGGIRAVGFVHSPLLKNKGTVCK
ELVHITDWYPTLISLAEGQIDEDIQLDGYDIWETISEGLRSPRVDILHNIDPYTPRQKMAPG
QQAMGSGTLQSSQSECSGTGNCLQEILATATGSPLSLSATWDRGTGTMNGSPCQLAKVYGFS
TSQPTHMRGWTYLTGIQES

Important Features:

Signal Peptide:

amino acids 1-37

Sulfatases signature 1.

amino acids 120-132

Sulfatases signature 2.

amino acids 168-177

Tyrosine kinase phosphorylation site.

amino acids 163-169

N-glycosylation sites.

amino acids 157-160, 306-309 and 318-321

FIGURE 44

CGGACGCGTGGGTGCGAGTGGAGCGGAGGACCCGAGCGGCTGAGGAGAGAGGAGGCGGCGGC
TTAGCTGCTACGGGGTCCGGCCGGCGCCCTCCCGAGGGGGGCTCAGGAGGAGGAAGGAGGAC
CCGTGCGAGAATGCCTCTGCCCTGGAGCCTTGCCTCCCCGTGCTGCTCTCCTGGGTGGCAG
GTGGTTTCGGGAACGCGGCCAGTGC AAGGCATCACGGTTGTTAGCATCGGCACGT CAGCCT
GGGGTCTGTCTACATATGGAAC TAAACTGGCCTGTCTGTACGGCTGGAGAAGAAACAGCAAGGG
AGTCTGTGAAGCTACATGCGAACCTGGATGTAAGTTTGGTGAGTGCCTGGGACCAACAAT
GCAGATGCTTTCCAGGATACACCGGGAACCTGCAGTCAAGATGTGAATGAGTGTGGAATG
AAACCCCGGCCATGCTCAACACAGATGTGTGAATACACACGGAAGCTACAAGTGCTTTTGCCT
CAGTGGCCATGCTCATGTCAGATGCTACGTGTGTGAAC TCTAGGACATGTGCCATGTATAA
ACTGT CAGTACAGCTGTGAAGACACAGAAGAAGGGCCACAGTGCCCTGTGTCCATCCTCAGGA
CTCCGCCTGGCCCCAAATGGAAGAGACTGTCTAGATATTGATGAATGTGCCTCTGGTAAAGT
CATCTGTCCCTACAATCGAAGATGTGTGAACACATT TGGGAAGCTACTACTGCAAAATGT CACA
TTGGTTTCGAAC TGCAATATATCAGTGGACGATATGACTGTATAGATATAAATGAATGTACT
ATGGATAGCCATACGTGCAGCCACCATGCCAATTGCTTCAATACCCAAGGGTCTTCAAGTG
TAAATGCAAGCAGGGATATAAAGGCAATGGACTTCGGTGTCTCTGCTATCCCTGAA AATTCTG
TGAAGGAAGTCTTCAGAGCACCTGGTACCATCAAAGACAGAATCAAGAAGTTGCTTGTCTCAC
AAAAACAGCATGAAAAAGAAGGCAAAAA TAAAAATGTTACCCCAAGACCCACGAGACTCC
TACCCCTAAGGTGAAC T TGCAGCCCTTCAACTATGAAGAGATAGTTTCCAGAGGCGGGAAC T
CTCATGGAGGTAAAAAGGGGAATGAAGAGAAATGGAAGAGGGGCTTGAGGATGAGAAAAGAG
AAGAGAAAGCCCTGAAGAATGACATAGAGGAGCGAAGCCCTCGAGGAGATGTGTTTTCCT
AAGGTGAATGAAGCAGGTGAATTTCGGCCTGATTCTGGTCCAAAGGAAAGCGCTAAC TCCAA
ACTGGAACATAAAGATTTAAATATCTCGTTGACTGCAGCTTCAATCATGGGATCTGTGACT
GGAAACAGGATAGAGAAGATGATTTTGACTGGAATCCTGCTGATCGAGATAATGTCTATTGGC
TTCTATATGGCAGTTCCGGCCTTGGCAGGT CACAAGAAAGACATTGGCCGATTGAAACTTCT
CCTACCTGACCTGCAACCCCAAAGCAACTTCTGTTTGCTCTTTGATTACCGGCTGGCCGGAG
ACAAAGTCGGGAAACTTCGAGTGTTTGTGAAAAACAGTAACAATGCCCTGGCATGGGAGAAG
ACCACGAGTGAGGATGAAAAGTGAAGACAGGGAAAAATTCAGTTGTATCAAGGAACTGATGC
TACCAAAAAGCATCATTTTGAAGCAGAACGTGGCAAGGGCAAAACCGGCGAAATCGCAGTGG
ATGGCGTCTGTCTTGTTCAGGCTTATGTCCAGATAGCCCTTTATCTGTGGATGACTGAATG
TTACTATCTTTATATTTGACTTTGTATGT CAGTTCCTCGGTTTTTTTGATATTGCATCATAG
GACCTCTGGCATTTTAGAATTACTAGCTGAAAAATTGTAATGTACCAACAGAAAAATTATTG
TAAGATGCCCTTCTGTATATAAGATATGCCAATATTTGCTTTAAATATCATATCACTGTATCT
TCTCAGTCATTTCTGAATCTTTCCNCATTATATATAAAATNTGGAANGTCAGTTTATCTC
CCCTCCTCNGTATATCTGATTGTATANGTANGTTGATGNGCTTCTCTCTACAAACATTTCTA
GAAAATAGAAAAAAAAGCAGAGAAATGTTTAACTGTTTGACTCTTATGATACTTCTTGA
AACTATGACATCAAAGATAGACTTTTGCCCTAAGTGCGCTAGCTGGGTCTTTCATAGCCAAAC
TTGTATATTAAATCTTTGTAATAATAA

FIGURE 45

MPLPWSLALPLLLSWVAGGFGNAASARHHGLLASARQPGVCHYGTKLACCYGWRRNSKGVCE
ATCEPGCKFGEVGPVGNKCRCFPGYTGKTCSDVNECGMKPRPCQHRCVNTHGSKYKCFCLSGH
MLMPDATCVNSRTCAMINCYSCEDTEEGPQCLCPSSGLRLAPNGRDCLDIDECASGKVICP
YNRRCVNTFGSVYYCKCHIGFELQYISGRYDCIDINECTMDSHTCSHHANCFNTQGSFKCKCK
QGYKGNGLRCSAIPENSVKEVLRAPGTIKDRIKLLAHKNSMKKKAKIKNVTPEPTRTPTPK
VNLQPFNYEEIVSRGGNSHGGKKGNEEK

Signal peptide:

amino acids 1-21

EGF-like domain cysteine pattern signature.

amino acids 80-91

Calcium-binding EGF-like domains

amino acids 103-124, 230-251 and 185-206

FIGURE 46

GGGAGCTGCTGCTGTGGCTGCTGGTGTCTGTGCGCGTCTCTCTGCTCTTGGTGCAGCTGCTG
CGCTTCTGAGGGCTGACGGCGACCTGACGCTACTATGGGCCGAGTGGCAGGGACGACGCC
AGAATGGGAGCTGACTGATATGGTGGTGTGGGTGACTGGAGCCTCGAGTGGAAATTGGTGAGG
AGCTGGCTTACCAGTTGTCTAAACTAGGAGTTTCTCTTGTGCTGTGAGCCAGAAGAGTGCAT
GAGCTGGAAGGGGTGAAAAGAAGATGCCTAGAGAATGGCAATTTAAAAGAAAAAGATATACT
TGTTTTGCCCCCTTGACCTGACCGACACTGGTTCCTCATGAAGCGGCTACCAAAGCTGTTCTCC
AGGAGTTTGGTAGAATCGACATTCTGGTCAACAATGGTGGAAATGCCAGCGTTCTCTGTGC
ATGGATACCAGCTTGGATGTCTACAGAAAGCTAATAGAGCTTAACTACTTAGGGACGGTGTCT
CTTGACAAAATGTGTTCTGCCTCACATGATCGAGAGGAAGCAAGGAAAGATTGTTACTGTGA
ATAGCATCCTGGGTATCATATCTGTACCTCTTCCATTGGATACTGTGCTAGCAAGCATGCT
CTCCGGGGTTTTTTTAATGGCCTTCGAACAGAACTTGCCACATACCCAGGTATAATAGTTTC
TAACATTTGCCCAGGACCTGTGCAATCAAATATTGTGGAGAATTCCCTAGCTGGAGAAGTCA
CAAAGACTATAGGCAATAATGGAGACCACTCCCAAGATGACAACCAAGTCGTTGTGTGCGG
CTGATGTTAATCAGCATGGCCAATGATTTGAAAGAAGTTGGATCTCAGAACCAACCTTTCTT
GTTAGTAACATATTTGTGGCAATACATGCCAACCTGGGCCTGGTGGATAACCAACAAGATGG
GGAAGAAAAGGATTGAGAACTTTAAGAGTGGTGTGGATGCAGACTCTTCTTATTTTAAATC
TTTAAGACAAAACATGACTGAAAAGAGCACCTGTACTTTTCAAGCCACTGGAGGGAGAAATG
GAAAACATGAAAACAGCAATCTTCTTATGCTTCTGAATAATCAAAGACTAATTGTGATTTT
ACTTTTAAATAGATATGACTTTGCTTCCAACATGGAATGAAATAAAAAATAAATAATAAAG
ATTGCCATGAATCTTGCAAAA

FIGURE 47

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA36343
><subunit 1 of 1, 289 aa, 1 stop
><MW: 32268, pI: 9.21, NX(S/T): 0
MVVWVTGASSGIGEELAYQLSKLGVSLVLSARRVHELERVKRRCLENGNLKEKDILVLPDL
TDTGSHEAATKAVLQEFGRIDILVNNQGMSQRSCLMDTSLDVYRKLIELNYLGTVSLTKCVL
PHMIERKQGKIVTVNSILGIISVPLSIGYCASKHALRGFFNGLRTELATYPGIIVSNICPGP
VQSNIVENSLAGEVTTKTIGNNGDQSHKMTTSRCVRLMISMANDLKEVWISEQPFLLVTYLW
QYMPTWAWWITNKMGGKRIENFKSGVDADSSYFKIFKTKHD

Important Features:

Signal Peptide:

amino acids 1-31

Transmembrane domain:

amino acids 136-157

Tyrosine kinase phosphorylation site.

106-113 and 107-114

Homologous region to Short-chain alcohol dehydrogenase

amino acids 80-90, 131-168, 1-13 and 176-185

FIGURE 48

GCGACGTGGGCACCGCCATCAGCTGTTTCGCGCGTCTTCTCCTCCAGGTGGGGCAGGGGTTTC
GGGCTGGTGGAGCATGTGCTGGGACAGGACAGCATCCTCAATCAATCCAAACAGCATATTCCG
TTGCATCTTCTACACACTACAGCTATTGTTAGGTTGCCTGCGGACACGCTGGGCCCTCTGTCC
TGA**TGCT**GTCTGAGCTCCCTGGTGTCCTCGCTGGTTCTGTCTACCTGGCCTGGATCCTGTTCT
TTCGTGCTCTATGATTCTCGATTGTTTGTATACCACTTATGTCTATCAAACGTGAGCCTGAT
GTGGCTCAGTTTCCGGAAGGTCCAAGAACCCAGGGCAAGGCTAAGAGGCACTGAGCCCTCA
ACCCAAGCCAGGGCTGACCTCATCTGCTTTGGTTTGGTCTTCAAGCCGCTCAGCGTGCTGTG
GACAGCGTGGCCCCGGCCCCCAAGCCTCAGGAGGGCAACACAGTCCCTGGCGAGTGGCCCC
TGGCAGGCCAGTGTGAGGAGCAAGGAGCCACATCTGCAGCGGCTCCCTGGTGGCAGACAC
CTGGGTCTCACTGCTGCCCACCTGCTTTGAAAAGGCAGCAGCAACAGAATGAATTCCTGGT
CAGTGGTCTTGGGTTCTCTGCAGCGTGAGGGACTCAGCCCTGGGGCCGAAGAGGTGGGGGTG
GCTGCCCTGCAGTTGCCAGGGCCTATAACCACTACAGCCAGGGCTCAGACCTGGCCCTGCT
GCAGCTCGCCACCCACAGCCACACACCCCTCTGCCTGCCCCAGCCCGCCCATCGCTTCC
CCTTTGGAGCCTCCTGCTGGGCCACTGGCTGGGATCAGGACACCAAGTATGCTCCTGGGACC
CTACGCAATCTGCGCCTGCGTCTCATCAGTCGCCCCACATGTAACTGTATCTACAACCAAGCT
GCACCAGCGACACCTGTCCAACCCGGCCCGGCTGGGATGCTATGTGGGGGCCCCCAGCCTG
GGGTGCAGGGCCCCCTGTCAAGGAGATTCCGGGGGCCCTGTGCTGTGCCTCGAGCCTGACGGA
CACTGGGTTCAGGCTGGCATCATCAGCTTTGCATCAAGCTGTGCCAGGAGGACGCTCCTGT
GCTGTGACCAACACAGCTGTCTACAGTTCCTGGCTGCAGGCTCGAGTTCAGGGGGCAGCTT
TCCTGGCCCCAGAGCCAGAGACCCCGGAGATGAGTGATGAGGACAGCTGTGTAGCCTGTGGA
TCCTTGAGGACAGCAGGTCCCCAGGCAGGAGCACCTCCCCATGGCCCTGGGAGGCCAGGCT
GATGCACCAAGGACAGCTGGCCTGTGGCGGAGCCCTGGTGTGAGAGGAGGCGGTGCTAACTG
CTGCCCACTGCTTCATTGGGCGCCAGGCCCCAGAGGAATGGAGCGTAGGGCTGGGGACCA
CCGAGGAGTGGGGCTGAAGCAGCTCATCCTGCATGGAGCCTACCCACCCCTGAGGGGGG
CTACGACATGGCCCTCTGTCTGCTGCCCCAGCCTGTGACACTGGGAGCCAGCCTGCGGCCCC
TCTGCCTGCCCTATCCTGACCACCACCTGCCTGATGGGGAGCGTGGCTGGGTTCTGGGACGG
GCCCGCCAGGAGCAGGCATCAGCTCCCTCCAGACAGTGCCCGTGACCCCTCTGGGGCCTAG
GGCCTGCAGCCGGCTGCATGCAGCTCCTGGGGGTGATGGCAGCCCTATTCTGCCGGGGATGG
TGTGTACCAAGTGTGTGGGTGAGCTGCCAGCTGTGAGGGCCTGTCTGGGGCACCACTGTGTG
CATGAGGTGAGGGGCACATGGTTCTTGGCCGGGCTGCACAGCTTCGGAGATGCTTGCCAAGG
CCCCGCCAGGCCGGCGGTCTTCAACCGCGCTCCTTGCCATGAGGACTGGGTGACAGTATTGG
ACTGCCAGGTCTACTTTCGCCGAGGAACAGAGCCCGAGGCTGAGCCTGGAAGCTGCCTGGCC
AACATAAGCCAACCAACCAGCTGCT**GAC**CAGGGGACCTGGCCATTCTCAGGACAAGAGAATGC
AGGCAGGCAAATGGCATTACTGCCCTGTCTCCCCACCCCTGTCAATGTGTGATTCCAGGCAC
CAGGCGAGGCCAGAAGCCAGCAGCTGTGGGAAGGAACCTGCCCTGGGGCCACAGGTGCCCA
CTCCCCACCCTGCAGGACAGGGGTGTCTGTGGACACTCCCAACCCAACTCTGCTACCAAGC
AGGCGTCTCAGCTTTCCTCCTCCTTACTCTTTTCAGATACAATCAGCCAGCCACGTTGTTT
TGAAAATTTCTTTTTTGGGGGGCAGCAGTTTTCTTTTTTAAACTTAAATAAATTTGTTAC
AAAAATAAA

FIGURE 49

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA40571

MLLSSSLVSLAGSVYLAWILFFVLYDFCIVCITTYAINVSLMWLSFRKVVQEPQKAKRHGNTV
PGEWPQASVRRQGAHICSGSLVADTWVLTAAHCFEKAAATELNSWSVVLGSLQREGLSPGA
EEVGVAALQLPRAYNHYSQGSIDLALLQLAHPTTHTPLCLPQPAHRFPFGASCWATGWDQDTS
DAPGTLRLNLRRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGPQPGVQGPCQGDSGGPVLC
LEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQARVQGAAFLAQSPTPEMSDEDS
CVACGSLRTAGPQAGAPSPWPWEARLMHQQLACGGALVSEEAVLTAAHCFIGRQAPEEWSV
GLGTRPEEWGLKQLILHGAYTHPEGGYDMALLLAQPVTLGASLRPLCLPYPDHHLDPDGERG
WVLGRARPGAGISSLQTVPTLLGPRACSRLLHAAPGGDGPILPGMVCTSAVGELPSCEGLS
GAPLVHEVRGTWFLAGLHSFGDACQGPAPPAVFTALPAYEDWVSSLDWQVYFAEEPEPEAEP
GSCLANISQPTSC

Important features:

Signal peptide:

amino acids 1-15

Homologous region to Serine proteases, trypsin family

amino acids 79-95, 343-359 and 237-247

N-glycosylation sites.

amino acids 37-40 and 564-567

Kringle domains

amino acids 79-96, 343-360 and 235-247

FIGURE 50

CGGGCCGCCCCGGCCCCCATTCGGGCCGGGCCTCGCTGCGCGGCGACTGAGCCAGGCTGG
GCCGCGTCCCTGAGTCCCAGAGTTCGGCGCGGCGCGGAGGGGAGCCCTTCCACCACGGGGAG
CCCAGCTGTGACCGCCTCACAGGAAGATGCTGCGTCGGCGGGGAGCCCTGGCATGGGTGT
GCATGTGGGTGCAGCCCTGGGAGCACTGTGGTTCTGCCTCAACAGAGCCCTGGAGGTCCAGG
TCCCTGAAGACCCAGTGGTGGCACTGGTGGGCACCGATGCCACCTGTGCTGCTCCTTCTCC
CCTGAGCCTGGCTTCAGCCTGGCACAGCTCAACCTCATCTGGCAGCTGACAGATACCAAACA
GCTGTGTGCACAGCTTTGCTGAGGGCCAGGACCAGGGCAGCGCCTATGCCAACCGCACGGCCC
TCTTCCCGGACCTGTCTGGCACAGGGCAACGCATCCCTGAGGCTGCAGCGCGTGCCTGTGGCG
GACGAGGGCAGCTTCACCTGCTTCGTGAGCATCCGGATTTCGGCAGCGCTGCCGTACGCCT
GCAGGTGGCCGCTCCCTACTCGAAGCCCAGCATGACCCTGGAGCCCAACAAGGACCTGCGGC
CAGGGGACACGGTGACCATCACGTGCTCCAGTACCAGGGCTACCTGAGGCTGAGGTGTTC
TGGCAGGATGGGCAGGGTGTGCCCTGACTGGCAACGTGACCACGTGCGAGATGGCCAACGA
GCAGGGCTTGTTTGTATGTGCACAGCGTCTGCGGGTGGTGTGGGTGCGAATGGCACCTACA
GCTGCCTGTGTGCGCAACCCCGTGTGTCAGCAGGATGCGCACRGTCTGTACCATCACAGGG
CAGCCTATGACATTCCCCCAGAGGCCCTGTGGGTGACCGTGGGGCTGTCTGTCTGTCTCAT
TGACTGCTGGTGGCCCTGGCTTTCTGTGTCTGGAGAAAGATCAAACAGAGCTGTGAGGAGG
AGAATGCAGGAGCTGAGGACCAGGATGGGGAGGGAGAAGGCTCCAAGACAGCCCTGCAGCCT
CTGAAACACTCTGACAGCAAAGAAGATGATGGACAAGAAATAGCCTGACCATGAGGACCAGG
GAGCTGCTACCCCTCCCTACAGCTCCTACCCCTGCGGTGCAATGGGGCTGCACTGTGAGCCC
TGCCCCAACAGATGCATCCTGCTCTGACAGGTGGGCTCCTTCTCCAAAGGATGCGATACAC
AGACCACTGTGCAGCCTTATTCTCCAATGGACATGATCCCAAAGTCATCCTGCTGCCTTTT
TTCTTATAGACACAATGAACAGACCACCCACAACCTTAGTTCTCTAAGTCATCCTGCCTGCT
GCCTTATTTACAGTACATACATTCTTAGGGACACAGTACACTGACCACATCACCAACCTC
TCTTTCAGTGCTGCGTGGACCATCTGGCTGCCCTTTTCTCCAAAGATGCAATATTTCAGA
CTGACTGACCCCTGCCTTATTTACCAAAGACACGATGCATAGTCACCCCGGCTTGTTC
TCCAATGGCCGTGATACACTAGTGATCATGTTTCAGCCCTGCTTCCACCTGCATAGAATCTTT
TCTTCTCAGACAGGGACAGTGC GGCTCAACATCTCCTGGAGTCTAGAAGCTGTTTCTTTC
CCCTCCTTCTCCTGCCCAAGTGAAGACAGGGCAGGGCCAGGAATGCTTTGGGGACACCG
AGGGGACTGCCCCCCACCCCCACCATGGTGCTATTCTGGGGCTGGGGCAGTCTTTCTGGC
TTGCCCTTGCCAGCTCCTGGCCTCTGGTAGAGTGAGACTTCAGACGTTCTGATGCCTTCGG
GATGTCATCTCTCCCTGCCCCAGGAATGGAAGATGTGAGGACTTCTAATTTAAATGTGGGAC
TCGGAGGGATTTGTAAACTGGGGGTATATTTTGGGGAAAATAAATGTCTTTGTAAAAA
AAAAAAAAAAAAA

FIGURE 51

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA41386

><subunit 1 of 1, 316 aa, 1 stop, 1 unknown

><MW: -1, pI: 4.62, NX(S/T): 4

MLRRRGSPGMGVHGAALGALWFCLTGALEVQVPEDPVVALVGTDATLCCSFSPPEPGFSLAQ
LNLIIWQLTDTKQLVHVSFAEGQDQGSAYANRTALFPDLLAQGNASIRLQRVRVADEGSFTCFV
SIRDFGSAAVSLQVAAPYSKPSMTLEPNKDLRPGDTVTITCSSYQGYPEAEVFWQDQGQGVPL
TGNVTTSQMANEQGLFDVHVSVLRVVLGANGTYSCLVRNPVLQQDAHXSVTITGQPMTFPPEA
LWVTVGLSVCLIALLLVALAFVCWRKIKQSCEEENAGAEDQDGEGEKSKTALQPLKHSDSKED
DGQEIA

Important features:

Signal peptide:

amino acids 1-28

Transmembrane domain:

amino acids 251-270

N-glycosylation site.

amino acids 91-94, 104-107, 189-192 and 215-218

Homologous region to Immunoglobulins and MHC

amino acids 217-234

FIGURE 52

TTCTGTGACCCTTGAGAAAAGAGTTGGTGGTAAATGTGCCACGTCTTCTAAGAAGGGGGAGTC
CTGAACCTTGTCTGAAGCCCTTGTCCGTAAGCCTTGAACCTACGTTCTTAAATCTATGAAGTCG
AGGGACCTTTTCGTGCTTTTGTAGGGACTTCTTTTCCCTTGCCTTCAGCAACATGAGGCTTTTTCT
TGTGGAAACGCGGTCTTGACTCTGTTTCGTCACTTCTTTGATTGGGGCTTTGATCCCTGAACCA
GAAGTGAAAATTGAAGTTCTCCAGAAGCCATTTCATCTGCCATCGCAAGACCAAAGGAGGGGA
TTTGATGTTGGTCCACTATGAAGGCTACTTAGAAAAGGACGGCTCCTTATTTCACTCCACTC
ACAAACATAACAATGGTCAGCCCATTTGGTTTACCCTGGGCATCCTGGAGGCTCTCAAAGGT
TGGGACCGAGGCTTGAAGGAATGTGTGTAGGAGAGAAGAGAAAGCTCATCATTCCTCCTGCTC
TCTGGGCTATGGAAGGAAGGAAAAGGTAATAATCCCCAGAAAAGTACACTGATATTTAATA
TTGATCTCCTGGAGATTCGAAATGGACCAAGATCCCATGAATCAITCCAGAAATGGATCTT
AATGATGACTGGAACCTCTCTAAAGATGAGGTTAAAGCATATTTAAAGAGGAGTTTGAAAA
ACATGGTGCGGTGGTGAATGAAAGTCATCATGATGCTTTGGTGGAGGATATTTTTGATAAAG
AAGATGAAGACAAAGATGGGTTTATATCTGCCAGAGAATTTACATATAAACACGATGAGTTA
TAGAGATACATCTACCCTTTTAAATAGCACTCATCTTTCAAGAGAGGGCAGTCATCTTTAA
AGAACATTTTATTTTATACAATGTTCTTTCTTGCTTTGTTTTTATTTTTTATATATTTTTT
CTGACTCCTATTTTAAAGAACCCCTTAGGTTTCTAAGTACCCATTTCTTTCTGATAAGTTATT
GGGAAGAAAAAGCTAATTGGTCTTTGAATAGAAGACTTCTGGACAATTTTTCACTTTCCACAG
ATATGAAGCTTTGGTTTACTTTCTCACTTATAAATTTAAAAATGTTGCACTGGGAATATACC
ACGACATGAGACCGGTTATAGCACAAAATAGCACCTTATATTTCTGCTTCCCTCTATTTTTCT
TCCAAGTTAGAGGTCAACATTTGAAAAGCCTTTTGCAATAGCCCAAGGCTTGCTATTTTCAT
GTTATAATGAATAGTTTATGTGTAAGTGGCTCTGAGTCTCTGCTTGAGGACCGAGGAAAA
TGGTTGTTGGACCTGACTTGTTAATGGCTACTGCTTTACTAAGGAGATGTGCAATGCTGAAG
TTAGAAAACAGGTTAATAGCCAGGCATGGTGGCTCATGCTGTAATCCAGCACTTTGGGAG
GCTGAGGCGGGCGGATCACCTGAGGTTGGGAGTTCGAGACCGCCTGACCACACCGGAGAAA
CCCTATCTCTACTAAAAATACAAAGTAGCCCGGCGTGGTGATGCGTGCTGTAATCCAGCT
ACCCAGGAAGGCTGAGGCGGCAGAAATCACTTGAACCCGAGGCCGAGGTTGCGGTAAGCCGAG
ATCACCTNAGCCTGGACACTCTGTCTCGAAAAAAGAAAAGAACCGGTTAATACCATATNA
ATATGTATGCATTGAGACATGCTACCTAGGACTTAAGCTGATGAAGCTTGGCTCTCTAGTGAT
TGGTGGCCTATTATGATAAATAGGACAAATCATTATGTGTGAGTTCTTTGTGAATAAAATG
TATCAATATGTTATAGATGAGGTAGAAAGTTATATTATATTCAATATTTACTTCTTAAGGC
TAGCGGAATATCCTTCTGGTCTTTAATGGGTAGTCTATAGTATATTATACTACAATAACA
TTGTATCATAAAGATAAAGTAGTAAACCAAGTCTACATTTTCCCATTTCTGTCTCATCAAAAAC
TGAAGTTAGCTGGGTGTGGTGGCTCATGCCGTGAATCCAGCACCTTTGGGGGCCAAGGAGGG
TGGATCACTTGAGATCAGGAGTTCAGACCCAGCCTGGCCCAACATGGTGAAACCTTGTCCTCTA
CTAAAAATACAAAAATAGCCAGGCGTGGTGGTGCAACCTGTAGTCCAGCTACTCGGGAG
GCTGAGACAGGAGATTTGCTTGAACCCGGGAGGCGGAGTTGCAGTGAGCAAGATTGTGCC
ACTGCACTCCAGCCTGGGTGACAGAGCAAGACTCCATCTCAAAAAAAGAAAGCAGAG
CCTACAGCAGCTACTATTGAATAAATACCTATCCTGGATT

FIGURE 53

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44194
><subunit 1 of 1, 211 aa, 1 stop
><MW: 24172, pI: 5.99, NX(S/T): 1
MRLFLWNAVLTLFVTSLIGALIPPEVKIEVLQKPFICHRKTGGDLMLVHYEGYLEKDGS
L
FHSTHKHNNQPIWFTLIGILEALKGWDQGLKGMCVGEKRLIIPPALGYGKEGKGKIPPE
ST
LIFNIDLLEIRNGPRSHESFQEMDLNDDWKLKDEVKAYLKKEFEKHGAVVNESHHDALVED
L
IFDKEDEKDGFIAREFTYKHDEL

Important features:

Signal peptide:

amino acids 1-20

N-glycosylation site.

amino acids 176-179

Casein kinase II phosphorylation site.

amino acids 143-146, 156-159, 178-181 and 200-203

Endoplasmic reticulum targeting sequence.

amino acids 208-211

FKBP-type peptidyl-prolyl cis-trans isomerase

amino acids 78-114 and 118-131

EF-hand calcium-binding domain.

amino acids 191-203, 184-203 and 140-159

S-100/ICaBP type calcium binding domain

amino acids 183-203

FIGURE 54

AATAAAGCTTCCTTAATGTTGTATATGTCTTTGAAGTACATCCGTGCATTTTTTTTTTAGCAT
CCAACCATTCCTCCCTTGTAGTTCTCGCCCCCTCAAATCACCCCTCTCCCGTAGCCCAACCGA
CTAACATCTCAGTCTCTGAAAATGCACAGAGATGCCTGGCTACCTCGCCCTGCCTTCAGCCT
CACGGGGCTCAGTCTCTTTTTCTCTTTGGTGCCACCAGGACGGAGCATGGAGGTACACAGTAC
CTGCCACCTCAACGTCTCAATGGCTCTGACGCCCGCCTGCCTTGCACCTTCAACTCCTGC
TACACAGTGAACCAAAACAGTTCTCCCTGAACTGGACTTACCAGGAGTGCACAACTGCCTC
TGAGGAGATGTTCTCCAGTTCCGATGAAGATCATTAACCTGAAGCTGGAGCGGTTTCAAG
ACCGCGTGGAGTTCTCAGGGAACCCAGCAAGTACGATGTGTCTGGTGTGCTGAGAAACGTG
GACCGGAGGATGAGGGATTACAACCTGCTACATCATGAACCCCTGACCGCCACCGTGG
CCATGGCAAGATCCATCTGCAGGTCTCATGGAAGAGCCCCCTGAGCGGACTCCACGGTGG
CCGTGATTGTGGGTGCTCCGTGCGGGGCTTCTGGCTGTGGTTCATCTGGTGTGATGGTG
GTCAAGTGTGTGAGGAGAAAAAAGAGCAGAAGCTGAGCACAGATGACCTGAAGACCGAGGA
GGAGGGCAAGACGGACGGTGAAGCAACCCGGATGATGGCGCCAAAGTAGTGGGTGGCCGGCC
CTGCAGCCTCCCGTGTCCCGTCTCCTCCCTCTCGCCCTGTACAGTGACCTGCCTGTCTGC
CTCTTGGTGTCTTCCGTGACCTAGGACCCAGGGCCACCTGGGGCTCCTGAACCCCG
ACTTCGTATCTCCACCTGCACCAAGAGTGACCCACTCTCTTCCATCCGAGAAACCTGCCA
TGCTCTGGGACGTGTGGGCCCTGGGGAGAGGAGAGAAAGGCTCCCACTGCCAGTCCCTGG
GGGGAGGCGAGGGCACATGTGAGGGTCCCCAGAGAGAAGGGAGTGGGTGGGCAGGGGTAGA
GGAGGGGCGCTGTCACTGCCCCAGTGTCTGCTGGCAGTGGCTTACAGAGAGGACCTGGTGG
GGAGGGAGGGCTTCTGTGTGTGACAGCGCTCCCTCAGGAGGGCTTGGCCTGGCACGGCTG
TGCTCCTCCCTGTCTCCAGCCCAGAGCAGCCATCAGGCTGGAGGTGACGATGAGTTCCTGA
AACTTGGAGGGGCATGTTAAAGGGATGACTGTGCATTCCAGGGCACTGACGGAAAGCCAGGG
CTGCAGGCAAACTGGACATGTGCCCTGGCCCAGGAGGCCATGTGGGCCCTCGTTTCCATT
GCTAGTGGCCTCCTTGGGGCTCCTGTTGGCTCCTAATCCCTTAGGACTGTGGATGAGGCCAG
ACTGGAAGACGATCTCAGGTAGGGGCCATGTTTCCAGCGGGACCCACCAACAGAGGCC
AGTTTCAAAGTCAGCTGAGGGGCTGAGGGGTGGGGCTCCATGGTGAATGCAGGTTGTGTCAG
GCTCTGCCTTCTCCATGGGGTAACCAACCTCGCCTGGGCAGGGGCAGCCAAGGCTGGGAAAT
GAGGAGGCCATGCACAGGGTGGGGCAGCTTCTTGGGGCTTCACTGAGAATCTCCCACTT
GCCCTTGTGGGGTTTCCACCTGGCTTTTGGCTACAGAGAGGGAAGGGAAAGCCTGAGGCCG
GCATAAGGGGAGGCCTTGGAACTGAGCTGCCAATGCCAGCCCTGTCCCATCTGCGGCCAGC
CTACTCGTCTCTCCCAACAACCTCCCTTCGTGGGGACAAAAGTGACAATTGTAGGCCAGGC
ACAGTGGCTCACGCTGTAACTCCAGCACTTGGGAGGCCAAGCGGGGTGATTACCTCCAT
CTGTTTAGTAGAAATGGGCAAAACCCATCTCTACTAAAAATACAAGAAATTAGCTGGGCGTG
GTGGCGTGTGCTGTAACTCCAGCTATTTGGGAGGCTGAGGCAGGAGAATCGCTTGAAGCCG
GGAAGCAGAGGTTGCAGTGAAGTGAAGTGTGATAGTGCCACTGCAATTCAGCCTGGGTGAC
ATAGAGAGACTCCATCTCAAAAAA

FIGURE 55

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45415

<subunit 1 of 1, 215 aa, 1 stop

<MW: 24326, pI: 6.32, NX(S/T): 4

MHRDAWLPRPAFSLTGLSLFFSLVPPGRSMEVTVPATLNVLNGSDARLPCTFNSCYTVNHKQ
FSLNWTYQECNNCSEEMFLQFRMKIINLKLERFQDRVEFSGNPSKYDVSVMRLRVQPEDEGI
YNCYIMNPPDRHRHGKIHQLVMEEPPEPDRSTVAVIVGASVGGFLAVVILVLMVVKCVRRK
KEQKLSTDDLKTEEGKTDGEGNPDDGAK

Important features:

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 161-179

Immunoglobulin-like fold:

amino acids 83-127

N-glycosylation sites.

amino acids 42-45, 66-69 and 74-77

FIGURE 57

TCACGGGGCTCATCTCTTTTTCTCTTTGGTGCCACCAGGACGAGCATGGAGGTNCACATA
CCTGCCACCCCTCAACGTCTCTCAATGGCTTTGACGCCCGCTGCCTGCACCTTCAACTCNG
CTACACAGTGAACCACAAACAGTTCTCCGTGAAGTGGATTATACCAGGAGTGCACAACTGGC
TCTGAGGAGATGTCTTCTCCAGTTCCTCCGATGGAAGATCATTTAAACCTGAAAGCTGGGAAGCGG
TTTTCAGAAGACCGCTGGAAGTTTCTCAGGGAACCCAGCAAGATCATGTGTCTGGTGATGC
TGAGAAACGTGCAGCGCGGAGATGAGGGAGATTTCACCTGCATCATCATGAACCCCC

TGGGGCGACGCTGCTACAACTGGGGCTCACCCTCCGCGCTACCGTGTGGGGCTGCTCCCGGATGGCTCCTGT
 TCTCTTCGTGCTAACTGCTGCGGACCCAGCGCTCCGCGCGAGCTGACCCCACTGGTGTGCTGCTC
 CTGGTGATTGGGTAACCAACTGGGAAGCAAGCTGGACAAGCCGACAGTGTGCATACCTCTCTCCAGGAAGA
 CCGAAGAGCTACTTCCAAATCTGGCTGAACTGGAAGCTGTCTGCTGCTGTCATCATCTGAGTGTGATTGACAAT
 TGAGGCTGGTTTACAAACAAATCAACGGGCGACCAAGTCTTCTGATGGTGGATGTAGCTGTGCTCGGCTTGT
 GGAAGAGCTCTCTCATGGATGTTCTGGACGCCACGAAGAAGCGGTGGGTCTCTTATTCTCACACATCTGGTGGAG
 GCGCTTGGGGCTGGGGTACACAGGGGTGAGATGTCCGAGGGGCTCCATGATGCTGGCGCGAGCCCCAAATG
 AAAACGGGCGCTTCTCTTGGCGCTCCGGAGATCTGAGGAGATGTACAAGCTGTATGGGGGGCGGCTGGTG
 TGGTGGTCCACAGTATGGGCAACATGTACACGCTTACTTCTGACGGCGAGCCGAGCGCTGGGAAGCAAGT
 ATATCCGGGCTCTCTGTGCTACGTGGTGCCTCTGGGGGGGCTGGCCACAGACGCTGTGCGCTCTGCTGTACGAG
 ACAACAAACCGGATCCAGTACTGGGCGCTTGAAGATCCGGGAGACAGCGGTGAGCTGTCTCCACAGCTGGC
 TGCTGCCCTAACATACATAGTCACTGAGAAGTGTCTGTGACAGACACCAATCACTACATACAGCTCGGG
 ATACCCAGAGTCTCTTCAGGATCACTGGCTTTGAAGATGTTCTGATCGGCAGGACACAGAAGGGCTGGTGG
 AAGCCACGATGCGCACTGGCGTGACCTGTGCATCTCTTATGGTATCTGGCGTCCCCACACAGACTCTCTACT
 ATGAGAGTCTCCCTGACGCTGACCTAAATCTGTCTTGGTGAACGGCGATGTACTGTGAATTTGAAGATGCC
 TGCAGTGGCGAGGCTGCCAGAGCCCGCAGGACCAAGTGTGCTCTCAGGAGCTGCCAGGCGAGCACATCG
 AGATGCTGGCCACGCCCACTCCCTGGCTACTGAAACCTGTGCTCTTGGGCTCGGACTCTCTGTGCCACAGGA
 CTCTCTGGGCTCGGCGCTGGAGCTGGCTTGGGCTCTGGGCGTGTATGGCCACGCGCTTTGCAAGATTTGTGA
 TCCACATTAAGGCGCCGAGTCTGTGACTGTGAAGCATCTGCCATGGGAAGTGCCTTTGTATCTTTCTCT
 GTGGGCTGAAGAAGGAAGAAATGAGAGTCTAGACTCAAGGGAACACTGGATGGCAAGAACTGCTGTATGGTGA
 ACTGCTGTGACTCTTAGAGCTGGCTCCAGGCTGAGCTGTGCGGCGCTGGTCCAGCTCCCTGCTGGGGCATGT
 TGTGCCCTATTCTGTGGCTTTTTCATCTGCTTGGCTACTGGGCGTGGCCCGAGCTCTTCTATGAGGATGTT
 ACTGGGCTGTGGTCTGTACCCAGAGTCCAGGAGATGGCTCTGCGCCCTCGGGTGGAGCTCTCCACACATCA
 GCGACAGATAGAGCTCGACTGTGTTCCAGGGCTGAGTCTGAGCTGTGCTTCCCTGTGGCTTACGCTGTGGCGAGCC
 TGACTGGCTCTCTGGGCGAGCTGTAGTACTCTTGACGGCAGGGCAGTTTGTGTGCTTCTGTCTGGTCCGAGC
 CTGGGACATCTCATCTCACTTACTCTCCCTTACACAGGAGCATCAAGCTCTGGATGGGGCAGAGATGTG
 CCCCAGCTCCGCGAGCTGTGTTCCAGGGCGCTGAGTTCTCGGATGTGCTATTGGCCCGAGACTGAAGTCTC
 CTCTCTTCACTCGGAGTGTGTTTCAAGGATGAGACGGGTTGTGAGCGATGGCTCTTGGAAACATATGGA
 GAAAGGGAATCCAAAGAGGACGCCAAGGCTGTCTCGAGCTCTCTCTGAGCTGCACTCTTGTCATACCCACATCA
 CACTGCGCACTGCCCTGAGGTTCTCATAGTACAAGTGGGTGACACAGGGCTGAGGATGGGGCTCTATTACCA
 CTGGGCAACGCCACCTTAGTGTGGGATGAGCCAGAAATCTGAATGGGACCTGAGAGAGCGAGGGGTCCCC
 TGGGCGCCCCTAGGGCTTCTGTGTGCCACGGGTGCTCATGAGTCTCCCTGTCAGGACAGGCTGAGAGAT
 CAGGGCTGCCATTATGGCAGTGAAGTCTAAGTGGGTGACTGCCACAGGCGAGAAGAGGTTACAGCTCTTAGT
 GGGGTTCCCAAGAAGCGCTTACGCTGGAGTCACTGAGTGTCTTCCACAGGGTTTCTGTGAGCAAGTATTCTCTG
 TGTGCATACGCTTGCATCTGTCTTCCCTTGTCTTCTGAGTGGCCCCACATGGGGCTCTGAGCAGGCTGTATCTGT
 GATTCTGCGCAATAAAGTACTCTGATGTGCTGTAAACAAAAAATAAAAAAATAAAAAA

FIGURE 59

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44189

><subunit 1 of 1, 412 aa, 1 stop

><MW: 46658, pI: 6.65, NX(S/T): 4

MGLHLRPYRVGLLPDGLLFLLLLLLMLLADPALPAGRHPVVLVPGDLGNQLEAKLDKPTVVH
YLCSKKTESYFTIWLNLLELLLPVIIDCWIDNIRLVYNKTSRATQFPDGVDRVPGFGKTFSL
EFLDPSKSSVGSYFHTMVESLVGWGYTRGEDVRGAPYDWRRAPNENGPYFLALREMI EEMYQ
LYGGFPVVLVAHSMGNMYTLYFLQRQPQAWKDKYIRAFVSLGAPWGGVAKTLRVLASGDNMRI
PVIGPLKIREQQRSAVSTSWLLPYNYTWSPEKVFVQTPTINYTLRDYRKFFQDIGFEDGWL
MQDTEGLVEATMPPGVQLHCLYGTGVPTPDSFYYESFPDRDPKICFGDGDGTVNLKSALQCQ
AWQSRQEBHQVLLQELPGSEHIEMLANATTLAYLKRVLG

Important features:

Signal peptide:

amino acids 1-28

Potential lipid substrate binding site:

amino acids 147-164

N-glycosylation sites.

amino acids 99-102, 273-276, 289-292 and 398-401

Lipases, serine proteins

amino acids 189-201

Beta-transducin family Trp-Asp repeat

amino acids 353-365

FIGURE 60

CGGACGCGTGGGCGGACGCGTGGGGCGGCGGCAGCGGCGGACGCGCGACATGGAGAGCGGG
GCCTACGGCGCGGCCAAGGCGGGCGGCTCCTTCGACCTGGCGCTTCCTGACGCAGCCGCA
GGTGTGGCGCGCGCCGTGTGCTTGGTCTTCGCCCTTGATCGTGTTCTCTGCATCTATGGTG
AGGGCTACAGCAATGCCACGAGTCTAAGCAGATGTACTGCGTGTCAACCGCAACGAGGAT
GCCTGCCGTATGGCAGTGCCATCGGGGTGCTGGCCTTCCTGGCCTCGGCCTTCTTCTGGT
GGTCGACGCGTATTTCCCCAGATCAGCAAACGCCACTGACCGCAAGTAACTGGTCATTGGTG
ACCTGCTCTTCTCAGCTCTCTGGACCTTCCTGTGGTTTGTGGTTTCTGCTTCTCACC AAC
CAGTGGGCAGTCACCAACCCGAAGGACGTGCTGGTGGGGGCGACTCTGTGAGGGCAGCCAT
CACCTTCAGCTTCTTTTCCATCTTCTCTGGGTGTGCTGGCCTCCCTGGCCTACCAGCGCT
ACAAGGCTGGCGTGGACGACTTCATCCAGAATTACGTTGACCCCACTCCGGACCCCAACT
GCCTACGCCCTCTACCCAGGTGCATCTGTGGACAACCTACCAACAGCCACCTTACCCAGAA
CGCGGAGACCACCGAGGGCTACCAGCCGCCCTGTGTACTTGAGTGGCGGTTAGCGTGGGAA
GGGGGACAGAGAGGGCCCTCCCTCTGCCCTGGACTTTCCTATCAGCCTCCTGGAAGTGCCA
GCCCCCTCTTTTACCTGTTCCATCCTGTGCAGCTGACACACAGCTAAGGAGCCTCATAGCC
TGGCGGGGCTGGCAGAGCCACCCCCAAGTGCTGTGCCCAGAGGGCTTCAGTCAGCCGCT
CACTCCTCCAGGGCACTTTTAGGAAAGGGTTTTTAGCTAGTGTTTTTCTCGCTTTTAATGA
CCTCAGCCCCGCTGCAGTGGCTAGAAGCCAGCAGGTGCCCATGTGCTACTGACAAGTGCT
CAGCTTCCCCCGGCCCGGTTCAGGCCGTGGGAGCCGCTATTATCTGCGTTCTCTGCCAAAG
ACTCGTGGGGCCATCACACTGCCCTGTGCAGCGGAGCCGACCAGGCTCTTGTGTCTCA
CTCAGGTTTGCTTCCCCTGTGCCCACTGCTGTATGATCTGGGGGCCACCACCTGTGCCGCT
GGCCTCTGGGCTGCCCTCCCGTGGTGTGAGGGCGGGCTGGTGCTCATGGCACTTCTCCTTG
CTCCACCCCTGGCAGCAGGAAGGGCTTTGCCTGACAACCCAGCTTTATGTAAATATTC
TGCAGTTGTTACTTAGGAAGCCTGGGGAGGGCAGGGTGCCCCATGGCTCCAGACTCTGTC
TGTGCCGAGTGATTATAAAATCGTGGGGGAGATGCCCGGCTGGGATGCTGTTTGGAGACG
GAATAAATGTTTTCTCATTCAAAG

FIGURE 61

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48304

<subunit 1 of 1, 224 aa, 1 stop

<MW: 24810, pI: 4.75, NX(S/T): 1

MESGAYGAAGAGGSFDLRRFLTQPQVVARAVCLVFALIVFSCIYGEGYSNAHESKOMYCVFN
RNEDACRYGSAIGVLAFLASAFFLVVDAYFPQISNATDRKYLVIQDLFLSALWTFWLVGFC
FLTNQWAVTNPKDVLVGADSVRAAITFSFFSIFSWGVLASLAYQRYKAGVDDFIQNYVDPTP
DPNTAYASYPGASVDNYQQPPFTQNAETTEGYQPPPVY

Important features:

Type II Transmembrane domain:

amino acids 1-45

Other transmembrane domains:

amino acids 74-90, 108-126 and 145-161

N-glycosylation site.

amino acids 97-100

FIGURE 62

GAGCCACCTACCCCTGCTCCGAGGCCAGGCCCTGCAGGGCCTCATCGGCCAGAGGGTGATCAGTGAGCAGAAGGATG
 CCCGTGGCCGAGGCCCCCCCAGGTGGCTGCGGGCAGGGGGACGGAGGTGATGGCCAGGGAAGCCGAGCAGAGGGG
 ATGTTTCAAGGCCCTGTGAGGACTCCAAGAGAAAGCCCGGGCTACCTCCGCTGTGGTCTGTTGTGCTGCTG
 GCCCTGCTGCTGCTGGCTTCGCGGGGGGTGCTACTCTGGTATTTCCTAGGTTACAAGGCGGAGGTGATGGTCAGC
 CAGGTGTACTCAGCAGCTCTGCGTGTACTCAATCGCCACTTCTCCAGAGTCTTACCCGCCGGGAATCTAGTGCC
 TTCCGCACTGAAACCGCCAAAGCCAGAGTGTCTCAAGAGCTCTACACAGCACCOCCTGGGAATCTACTAC
 AACTCCAGCTCCGCTCTTCTTCTTGGGAGGGACCCCTCACCTGCTTCTTCTGGTTCATTCTCCAAATCCCCGAG
 CACCGCCGCTGATGCTCCAGGCCCGAGGTGGTGCAGGCACTGCTGGTGGAGAGCTGCTGTCCACAGTCAACAGC
 TCGCTGCGCTCCCTACAGGCCCGAGTACGAAGTGGACCCCGAGGGCCTAGTGATCTCTGGAGCCAGGTGTGAAA
 GACATAGCTGCATTGAATTCCACGCTGGTGTGTTACCGCTACAGCTACGTGGGCCAGGGCCAGGTCTCTCCGGCTG
 AAGGGGCTTGACCACTCTGGCCTCAGCTGCTGTGGCACTCTCAGGGCCCCCAAGGACCTCATGCTCAAACTCCGG
 CTGGAGTGGAGCCTGGCAGAGTGCCGGGACCGACTGGCCATGTATGACGTGGCCGGGCCCTCGAGAAAGAGGCTC
 ATCACTCTCGGTGTACGGCTGCAGCCGCGCAGGAGCCCGTGGTGGAGGTTCTGGCGCTGGGAGGCCATCATGGCGTCT
 GTCTGGAAGAAGGGCCTGCACAGCTACTACGACCCCTTCGTGCTCTCCGTGCAGCCGGTGGTCTTCCAGGCCCTGT
 GAAGTGAACCTGACGCTGGACAACAGGCTCGACTCCAGGGCGTCTCAGCACCCCGTACTTCCCCAGCTACTAC
 TCGCCCCAAACCCACTGCTCTCTGGCACTCAGGTGCCCTCTCTGGACTACGGCTTGGCCCTCTGGTTTGTATGCC
 TATGCACTGAGGAGGCAGAAGTATGATTTCGGTGCACCCAGGGCCAGTGGACGATCCAGAACAGGAGGCTGTGT
 GGCTTGGCATCCTTGACGCCCTACGCCGAGAGGATCCCGTGGTGGCCACGGCCGGGATCACCATCACTTCACC
 TCCAGATCTCCCTCACCGGGCCCGGTGTGCGGGTGCACTATGGCTTGTACAACAGTGGAGCCCCCTGCCCTGGA
 GAGTTCTCTGTCTGTGAATGGACTCTGTGTCCTTGCTGTGATGGGGTCAAGGACTGCCCAACGGCTGGAT
 GAGAGAACTGCGTTTGCAGAGCCACATTCAGTGCAAAGAGGACAGCACATGCATCTCACTGCCCAAGGTCTGT
 GATGGGCGCCTGATTGTCTCAACGGCAGOGATGAAGAGCAGTGCCAGGAAGGGGTGCCATGTGGGACATTCAAC
 TTCCAGTGTGAGGACCGGAGCTGCGTGAAGAAGCCAAACCCGAGTGTGATGGGGGCCCGACTGCAGGGACGGC
 TCGGATGAGGAGCACTGTGACTGTGGCTCCAGGGCCCCCTCAGCCGCAATTGTTGGTGGAGCTGTGCTCTCGAG
 GGTGAGTGGCCATGGCAGGCCAGCTCCAGGTTTCGGGGTCGACACATCTGTGGGGGGGCCCTCATGCTGACCGC
 TGGGTGATAACAGCTGCCCATGCTCTCCAGGAGGACAGCATGGCCCTCCACGGTGTGTGGACCCGTGTTCTGGGC
 AAGGTGTGGCAGAATCGCGCTGGCTGGAGAGGTGTCTTCAAGGTGAGCCGCGCTGCTGCTGCACCCCGTACAC
 GAAGAGGCAGCCATGACTACGAGCTGGCGCTGCTGCAGCTCGACCAACGGCTGTGCGCTCGGCCGCGCTGCGC
 CCGTGTGCTGCTGCCGCGCTGCCACTTCTCGAGCCCGGCTGCACTGCTGGATTACGGGCTGGGGCGCCTTG
 CGCGAGGGCGGCCCATCAGCAACGCTCTGCAGAAAGTGATGTGCAGTTGATCCACACAGGACTGTGCAGCGAG
 GCTATCGTACCAAGGTGACGCCACGCTGCTGTGTGCGGCTACCGCAAGGGCAGGAAGGATGCTGTGACGGT
 GACTCAGGTGTGCTGCTGCTGTGTCAGGCCACTCAGTGCCGCTGGTCTTGGCGGGCTGTGTCAGCTGGGGCTG
 GCGTGTGGCGGGCTTAATCTACTTCGGGCTCTACCCGCTACAGGCTGTGATCAGCTGGATCCAGCAAGTGGT
 ACTCTGGCAACTCTGCCCTCTGCAGGCGGCCCACTCTCGACTCAGAGAGCCAGGGCACTCTGCCAAGCAGG
 GGGACAGTATTCTGGCGGGGGTGGGGAGAGAGCAGGCCCTGTGGTGGCAGGAGGTGGCATCTTCTGCTCGT
 CTGATCTCTGCTCCAGTGTGTCAGGAGGATGGAGAAGTGCCAGCAGCTGGGGGTCAAGACGTCCCTCGAGGACC
 CAGGCCACACCCAGCCCTTCTGCTCCCAATTTCTCTCTCTCCCTCCCTCTCTCCACTGCTCTAATGCAAG
 GCAGTGGCTCAGCAGCAAGAATGTGTTCTACATCTCCGAGGAGTGTCTGAGGTGCGCCCCACTCTGTACAGAGG
 CTGTTTGGGCGCCTTGCTCCAGAGAGCAGATCCAGCTCTGGAAAGCCCTGGCTCAACTTGGGATCTGGGAAT
 GGAAGGTGCTCCCATCGAGGGGACCCCTCAGAGCCCTGGAGACTGCAGGTGGGCTGCTGCCACTGTGGAACGA
 AAGGTGGGGAAGTCTTGAATCAGGCTCTTGCCCAACCCCTGCTGCCACTTGGGCTCAGAGCCAGACCCCT
 CACTGGGAGGTGAGCTCAGTCCCTTTGGAATAAAGTGCCTGATCAAAAAA

1007336-1007337

FIGURE 63

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49152
><subunit 1 of 1, 802 aa, 1 stop
><MW: 88846, pI: 6.41, NX(S/T): 7
MPVAEAPQVAGGQGDGGEGEEAEPGGMFKACEDSKRKARGYLRLVPLFVLLALLVLASAGVL
LWYFLGYKAEVMVSQVYSGSLRVLNHRHFSQDLTRRESSAFRSETAKAQKMLKELITSTRLGT
YNNSSSVYSFGEGPLTCFFWFILQIPEHRRMLMSPEVVQALLVEELLSTVNSSAAVPYRAEY
EVDPEGLVILEASVKDIAALNSTLGCYRYSYVGQGVRLRKGPDLHLASSCLWHLQGPDLML
KLRLWTLAECDRLAMVDVAGPLEKRLITSVYGCSRQEPVVEVLASGAIMAVVWKKGLHSY
YDPFVLSVQPVVQACEVNLTLNRLDSQGVLTSPYFSPSYSPQTHCSWHLTVPSLDYGLAL
WFDAYALRRQKYDLPCQTQGWTIQNRRLCGLRILQPYAERIPVVATAGITINFTSQISLTGP
GVRVHYGLYNQSDPCPGEFLLCSVNGLCVPACDGVKDCPNGLDERNVCVRATFQCKEDSTCIS
LPKVCDDGQPDCLNGSDDEEQCQEGVPCTFTFQCEDRSCVKKPNPQCDGRPDGSDSEEHCD
CGLQGPSSRIVGGAVSSEGEVWPQASLQVRGRHICGGALIDRWVITAAHCFQEDSMASVTL
WTVFLGKVVQNSRWPGEVSFKVSRLLLHPYHEEDSHDYDVALQLDHPVVRSAVRPVCLPA
RSHFFEPGLHCWITGWGALREGGPISNALQKVDVQLIPQDLCSEAYRYQVTPRMLCAGYRKG
KKDACQGDSSGGLVCKALSGRWFLAGLVSWGLGCGRPNYFGVYTRITGVISWIIQQVVT

Important features:

Type II transmembrane domain:

amino acids 46-67

Serine proteases, trypsin family, histidine active site.

amino acids 604-609

N-glycosylation sites.

amino acids 127-130, 175-178, 207-210, 329-332, 424-427, 444-447
and 509-512

Kringle domains.

amino acids 746-758 and 592-609

Homologous region to Kallikrein Light Chain:

amino acids 568-779

Homologous region to Low-density lipoprotein receptor:

amino acids 451-567

FIGURE 64

GCACCCAGGCCAGTGGACGATCCAGAACAGGAGGCTGTGTGGCTTGC GCATCCTGCAGCCC
TACGCCGAGAGGATCCCCGTGGTGGCCACGGCCGGGATCACCATCAACTTCACCTCCAGAT
CTCCCTCACGGGCCCGGTGTGCGGGTGCACTATGGCTTGTACAACCAGTCCGACCCCTGCC
CTGGAGAGTTCCTCTGTTCTGTGAATGGACTCTGTGTCCCTGCCTGTGATGGGGTCAAGGAC
TGCCCCAACGGCCTGGATGAGAGAAAAGTGGCTTGCAGAGCCACATTCAGTGCAAGAGGA
CAGCACATGCATCTCACTGCCAAGGTCTGTGATGGGCAGCCTGATTGTCTCAACGGCAGCG
ATGAAGAGCAGTGCCAGGAAGGGGTGCCATGTGGGACATTACCTTCCAGTGTGAGGACCGG
AGCTGCGTGAAGAAGCCCAACCCGCAGTGTGATGGGCGGCCGACTGCAGGGACGGCTCGGA
TGAGGAGCACTGTGACTGTGGCCTCCAGGGCCCCCTCCAGCCGATTGTTGGTGGAGCTGTGT
CCTCCGAGGTGAGTGGCCATGGCAGGCCAGCCTCCAGGTTGCGGGTCGACACATCTGTGGG
GGGGCCCTCATCGCTGACCGTGGGTGATAACAGCTGCCCACTGCTTCCAGGAGGACAGCAT
GGCCTCCACGGTGCTGTGGACCGTGTTCTTGGGCAAGGTGTGGCAGAACTCGCGCTGGCCTG
GAGAGGTGTCTTCAAGGTGAGCCGCCTGCTCCTGCACCCGTACCAAGAGGACAGCCAT
GACTACGACGTGGCGCTGCTGCAGCTCGACCACCCGGTGGTGCCTCGGCCGCCGTGCGCCC
CGTCTGCTGCCCCGCGCTCCCACTTCTTCGAGCCCGGCTGCAGTGTGTTGATTACGGGCT
GGGGCGCCTTGCGCGAGGGCGGCCCATCAGCAACGCTCTGCAGAAAGTGGATGTGCAGTTG
ATCCCAAGGACCTGTGCAGCGAGGCCTATCGCTACCAGGTGACGCCACGCATGCTGTGTGC
CGGCTACCGCAAGGGCAAGAAGGATGCCGTGTGAGGGTCACTCAGGTGGTCCGCTGGTGTGCA
AGGCACTCAGTGGCCGCTGGTTCTTGGCGGGGCTGGTCAGCTGGGGCCTGGGCTGTGGCCGG
CCTAACTACTTTCGGCGTCTACACCCGCATCACAGGTGTGATCAGCTGGATCCAGCAAGTGT
GACCTGAGGAACTGCCCCCTGCAAAGCAGGGGCCACCTCCTGGACTCAGAGAGCCCAGGGC
AACTGCCAAGCAGGGGGACAAGTAT

Figure 1. Schematic representation of the experimental design. The subjects were divided into two groups: the control group (CG) and the experimental group (EG). The CG was divided into two subgroups: the control group (CG) and the control group (CG). The EG was divided into two subgroups: the experimental group (EG) and the experimental group (EG). The CG was divided into two subgroups: the control group (CG) and the control group (CG). The EG was divided into two subgroups: the experimental group (EG) and the experimental group (EG).

[illegible]

FIGURE 66

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49646

><subunit 1 of 1, 354 aa, 1 stop

><MW: 39362, pI: 8.35, NX(S/T): 2

MSNSVPLLCFWSLCYCFAAGSPVFPFGPEGRLEDKLHKPKATQTEVKPSVRFNLRSTSKDPEHE
GCYLSVGHSQPLEDCSFNMTAKTFFIIHGWTMSGIFENWLHKLVSALHTREKDANVVVVDWL
PLAHQLYTDVNNTRVVGHISIARMLDWLQEKDDFSLGNVHLIGYSLGAHVAGYAGNFVKGTV
GRITGLDPAGPMFEGADIHKRLSPDDADFVDVLHTYTRSFGLSIGIQMPVGHIDIYPNGGDF
QPGCGLNDVLGSIAYGTITEVVKCEHERAVHLFVDSL VNQDKPSFAFQCTDSNRFKKGICLS
CRKNRCNSIGYNAKMRNKRNSKMYLKTRAGMPFRGNLQSLECP

Important features:

Signal peptide:

amino acids 1-16

Lipases, serine active site.

amino acids 163-172

N-glycosylation sites.

amino acids 80-83 and 136-139

FIGURE 67

CGGACGCGTGGGCGGACGCGTGGGCCTGGGCAAGGGCCGGGGCGCCGGGCCGAGCCACCTCTTCCCCCTCCCCCGC
TTCCTCTGTGCGCTCCGCTGGCTGGACGCGCTGGAGGAGTGGAGCAGCACCCCGCCGGCCCTGGGGGCTGGACAGT
CGGCCAAGTTTGGCCGAAGAGGAAAGTGGTCTCAAAACCCGCGCAGGTGGCCGACAGGCGCAGACCAGGGCGCTCG
CTGCTTGCGGGGCGGGCTGTATGGCGAGGGCCGCGCCCCAGTGCAGAGACCCGGGGCTTCAAGAGCCGCGCCGGGAG
AGAAGAGTCCGGCGCGGACGAGGAAAAACAACTCCAAAGTTGGCGAAAGGACCGGCCCTACTCTCCGGGCTGCGG
CCGCTTCCCGCCCCCAGCCCTTGGCATTCCAGAGTACGGGTCCGAGCCCGGGCCATGGAGCCCCCTTGGGGAGGCGG
CACCAGGAGGCTGGGCGCCCGGGGCTCCGCGCGACCCCATCGGGTAGACCACAGAAAGCTCCGGGACCCCTTCGG
GCACCTCTGGACAGCCCGAGGATGGTGGCCACCTCTCTCTCTCTCTCTTGGAGGCGCTCTGGCCATCCAG
ACCGGATATTTTCCAAATCATGCTTGTGAGGACCCCGCAGCAGTGTCTTAGAAGTCGAGGGCACCTTACAGA
GGCCCCGTGTGGGGACAGCCGCACTCCCTTGCCAACTGCACCTGGCTCATCTGGGAGCAAGGAACAGACATG
TCAACATCAGGTTCCAGAAGCTACACCTGGCTGTGGCTCAGAGCGCTTAAACCTACGCTCCCTCTCCAGCCAC
TGATCTCCCTGTGTGAGGCACTCCAGCCCTCTGCAGCTGCCCGGGGGCAAGCTCACCATCACTTACAGCTATG
CTGGGGCCAGAGCACCCATGGGCCAGGGGCTTCTGCTCTCTACAGCCAAAGATTGGCTGATGTGCTTGCAGGAAG
AGTTTCAGTGCCGAAACACCCGCTGTGATCTGCTGTCCAGCGCTGTGATGGGGTTGATGCCCTGGCGATGGCT
CTGATGAAGCAGGTTGCAGCTCAGACCCCTTCCCTGGCTGACCCCAAGACCCGCTCCCTCCCTGCTTGCAGT
TCACTTGGAGGACTTCTATGGGGTCTTCTCTCTCTCTGGATATACACACCTAGCCTCAGTCTCCACCCCCAGT
CCTGCCATTGGCTGTGGACCCCCATGATGGCCGGCGGCTGGCCGTGCGCTTACAGCCCTGGACTTGGGCTTTG
GAGATGCAGTGCATGTGTATGACGGCCCTGGGCCCTTGAGAGCTCCCGACTACGCTAGTCTACACCCACTTCA
GCAATGGCAAGGCTGTCACTGTGAGACACTGTCCTGGCCAGGCTGTGTGCTTACACACAGTGTGCTTGGAGCA
ATGGTCTGTGGCTTCAATGCCACCTACCATGTGCGGGGCTATTGCTTGGCTTGGGACAGACCTGTGGCTTAGGCT
CTGGCTGGGAGCTGGCGAAGGCTTAGGTGAGCGCTGCTACAGTAGGACACAGCGCTGTGACGGCTCATGGGACT
GTGCTGACGGCACAGATGAGGAGGACTGCCAGGCTGCCACCTGGACACTTCCCTGTGGGGCTGCTGSCACCT
CTGGTGCCACAGCTGCTACCTGCTGCTGACCGCTGCAACTACAGACTTCTGTGCTGATGGAGCAGGATGAGA
GACGCTGTGCGCATTGCAGCTTGGCAATTTCCGATGCGGGACAGAGAAGTGGTGTATGAGACGTGGGCTGTGG
ATGGGCAGCCAGACTGTGCGGACGGCAGTGATGAGTGGGACTGCTCTATGTTCTGCCCCGCAAGTCTATACAG
CTGCAGTCTTGGCAGCCTAGTGTGCGGCTGCTCTGCTGATCGCTGGGCTGCACTGCAAGCTCTATGCCA
TTGCAACCCAGGAGTACAGCATCTTGGCCCCCTCTCCCGATGGAGGCTCAGATTGTGACAGCAGCAGGCCCCC
CTTCACTGTGCTCATTGCTCCAGGGTGCCATCCACCTGTAGAAGACTTTCCTACAGGAATCCTAATGATA
ACTCACTGTCTGGCACTTGCCTTCTGCTACAGACTTACGCCAGGATGATGACTCAGGAGGTGGCCAGGTG
CCGCGCTGCTCAGCGGGGCCCTTGTATCGACGCTGTGATCGCGCTCCGCGGCTGGGGCTGTCTCTCTCGAA
CCAACACCCCGGCTGGGCTCTGAGGCGAGATCCAGGTCAACACTCTGCTGCTGCTCCCTTGGAGGCCATGATG
GTGGCACAGGTCAGGCCCTGAGGGCGGGCAGTGGGTGGGCAAGATGGGAGCAGGACCCCCACTGCCCATCA
AGCTCCCTCCCATCTGCTAGCAGCTCTCAGGCCCACTACTGCTCCCTGAAGCCCCAGGGGCACTGCCCTCAC
TGGCCCTAGAGCCATCACTATTGTCTGAGTGGTGCAGGCCCTGCGAGGCCGCGCTGTTGCCAGCCTGGGGCCCC
CAGGACCAACCCGAGGCCCCCTGGACCCCAACAGCAGTCTCTGGCCCTGGAAGATGAGGACGATGTGCTACTGG
TGCCACTGGCTGAGCCGGGGGTGGGTAGCTGAGGCGAGAGGATGAGCCACTGCTTACCTGAGGGGACCTGGGG
CTCTACTGAGGCTCTCCCTGGGGGCTCTACTCATAGTGCGACAACCTTTAGAGGTGGGTGAGCTCCCTCC
ACCATTCTCTCTCTGCTGCTGATTTGAGGAGCTTGGTGGGCTCCCGTTGACCTCATGTAGCTGCTATAAAGT
TAAGTGTCCCTCAGGCGAGGAGAGGGCTCAGAGAGTCTCTCTGTACGTGGGCGGACAGACACCCAGTCCCT
TCACCAACCACTGCTCCCAAGCCACCACTATTGGTGGCTGTTTTTAAAAAGTAAAGTCTTAGAGGATCATA
GGTCTGGACACTCTCTTGCCAAACCTTACCCAAAGTGGCTTAAAGCACCGGAATGCCAATTAACTAGAGA
CCCTCCAGCCCCAAGGGGAGGATTTGGGCAGAACCTGAGGTTTTGGCATCCCAATCCCTCTCAGGGGCTGG
CTCACAAAAGAGTGCAACAAATGCTTCTATTCCATAGCTACGGCATTGCTCAGTAAGTTGAGGTCAAAAATAAA
GGATCATACATCTC

FIGURE 68

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49631

<subunit 1 of 1, 713 aa, 1 stop

<MW: 76193, pI: 5.42, NX(S/T): 4

MLLATLLLLLLGGALAHDPRIIFPNHACEDPPAVLLEVQGTQRPLVRDSRTSPANCTWLIL
GSKEQTVTIRFQKLHLACGSERLTLRSPLQPLISLCEAPPSPQLPGGNVTITYSYAGARAP
MGQGFLLSYSQDWLMCLQEEFQCLNHRCSVSAVQRCDGVDACGDGSDGSSDPFPGLTFRP
VPSLPCNVLTLEDFYGVFSSPGYTHLASVSHPQSCHWLLDPHDGRRLAVRFTALDLGFDAVH
VYDGPGPPESSRLLRSLTHFSNGKAVTVETLSGQAVVSYHTVAWSNGRGFNATYHVRGYCLP
WDRPCGLSGSLGAGEGLGERCYSEAQRCDGSWDCADGTDEEDCPGCPPGHFPCGAAGTSGAT
ACYLPADRCNYQTFCADGADERRCRHCQPGNFRCRDEKCVYETWVCDGQPDGSDGSEWDCS
YVLPKRVITAAVIGSLVCGLLLVIALGCTCKLYAIRTQEYSIFAPLSRMEAEIVQQAPP
SYGQLIAQGAIPPVEDFPTENPNDNSVLGNLRSLQLILRQDMTPGGGPGARRRQRGRLMRRLVR
RLRRWGLLPRTNTPARASEARSQVTPSAAPLEALDGGTGPAREGGAVGGQDGEQAPPLPIKA
PLPSASTSPAPTTVPAPGPLPSLPLEPSLLSGVVQALRGRLLPGLPGPPTRSPPGPHTAV
LALEDEDDVLLVFLABPGVWVAEAEDEPLLT

Important features:

Signal peptide:

amino acids 1-16

Transmembrane domain:

amino acids 442-462

LDL-receptor class A (LDLRA) domain proteins

amino acids 411-431, 152-171, 331-350 and 374-393

FIGURE 69

CGAGCTGGGCGAGAAGTAGGGGAGGGCGGTGCTCCGCCGCGTGGCGGTTGCTATCGCTTCG
CAGAACCTACTCAGGCAGCCAGCTGAGAAGAGTTGAGGGAAAGTGCTGCTGCTGGGTCTGCA
GACGCGAATGGATAACGTGCAGCCGAAAAATAAACATCGCCCTTCTGCTTCAGTGTGAAAGG
CCACGTGAAGATGCTGCGGCTGGCACTAACTGTGACATCTATGACCTTTTTTATCATCGCAC
AAGCCCCGAACCATATATTGTTATCACTGGATTGGAAGTACCGTTATCTTATTTTTTCATA
CTTTTATATGTACTCAGACTTGATCGATTAAATGAAGTGGTTATTTTGGCCTTTGCTTGATAT
TATCAACTCACTGGTAACAACAGTATTTCATGCTCATCGTATCTGTGTTGGCACTGATACCAG
AAACCACAACATTGACAGTTGGTGGAGGGGTGTTGCACTTGTGACAGCAGTATGCTGTCTT
GCCGACGGGGCCCTTATTTACCGGAAGCTTCTGTTCAATCCAGCGGTCCCTTACCAGAAAAA
GCCTGTGCATGAAAAAAGAAGTTTTGTTAATTTTATATTACTTTTTAGTTTGATACTAAGT
ATTAAACATATTTCTGTATTCTTCAAAAAAAAAAAAAAAAAA

FIGURE 70

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49645

><subunit 1 of 1, 152 aa, 1 stop

><MW: 17170, pI: 9.62, NX(S/T): 1

MDNVQPKIKHRPFCFSVKGHVKMLRLALTVTSMTFFIIAQAPEPYIVITGFVTVILFFILL
YVLRDLRLMKWLFWPLLDIINSLVTTVFMLIVSVLALIPETTTTLTVGGGVFALVTAVCCLAD
GALIYRKLLFNPSGPYQKKPVHEKKEVL

Important features:

Potential type II transmembrane domain:

amino acids 26-42

Other potential transmembrane domain:

amino acids 44-65, 81-101 and 109-129

Leucine zipper pattern

amino acids 78-99 and 85-106

N-myristoylation site.

amino acids 110-115

Ribonucleotide reductase large subunit protein

amino acids 116-127

GGGCGAGAAGTAGGGAGGGCGTGTTCCGCCGCGGTGGCGGTTGCTATCGTTTTGCAGAACC
TACTCAGGCAGCCAGNTGAGAAGAGTTGAGGGAAAGTGCTGCTGCTGGGTCTGCAGACGCGA
TGGATAACGTGCAGCCGAAATAAAACATCGCCCTTCTGC'TTCAGTGTGAAGGCCACGTG
AAGATGCTCGGGCTGGCACTAACTGNGACATCTATGACCTTTTTTATNATCGCACAGCCCC
TGAACCATATATTGTTATCACTGGATTGAAAGTCAACGTTATCTTATTTTTTCATACCTTTTAT
ATGTACTCAGACTTGATCGAATTAATGAAGTGGTTATTTTTGGCCCTTTGCTTGATATTATCAAC
TCTACTGGTAAACAACAGTATTCATGCTCATCGGTATCTGTGTTGGCATGATACAGAAACCA
AACATTGCAGCTTGGTGGAGGGGTGTTTGCACITGTGCAGCAGCATGCTGTGNTTGGCGAC

FIGURE 72

CAGCCCCGCGCGCCGCCGAGTCGCTGAGCCGCGGCTGCCGGACGGGACGGGACCGGCTAGG
CTGGGCGCGCCCCCGGGCCCCGCCGTGGGCATGGGCGCACTGGCCCCGGGCGCTGCTGCTGC
CTCTGCTGGCCCACTGGCTCCTGCGCGCCGCCCGGAGCTGGCCCCCGCGCCCTTCACGCTG
CCCCCTCCGGGTGGCCGCGGCCACGAAACCGCGTAGTTGCGCCACCCCGGGACCCGGACCCC
TGCCGAGCGCCACGCGCGCGGCTTGCGCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGG
GCGCGCCCAACTTCTTTGGCCATGGTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTAC
CTGGAGATGCTGATCGGGACCCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAG
TAACTTTTGCGTGGCAGGAACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGT
CTAGCACATACCGCTCCAAGGGCTTTGACGTACAGTGAAGTACACAAGGAAGCTGGACG
GGCTTCGTTGGGAAGACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTGTCAA
CATTGCCACTATTTTTGAATCAGAGAATTTCTTTTGGCCTGGGATTAATGGAATGGAATAC
TTGGCCTAGCTTATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCC
CTGGTGACACAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGGC
CGTTGCTGGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGT
ATAAAGGAGACATCTGGTATACCCCTATTAAAGGAAGAGTGGTACTACCAGATAGAAATTCTG
AAATTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGC
CATCGTGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTATGCGGTGGTGG
AAGCTGTGGCCCGCGCATCTCTGATTCAGAATTCTCTGATGGTTTCTGGACTGGGTCCCAG
CTGGCGTGCTGGACGAATTTCGGAAACACCTTGGTCTTACTTCCCTAAATCTCCATCTACCT
GAGAGACGAGAACTCCAGCAGGTCAATCCGTATCACAATCTCGCTCAGCTTTACATTACAGC
CCATGATGGGGGCCGCGCTGAATTATGAATGTTACCGATTGGGCATTTCCCCATCCACAAAT
GCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCACTTTCGACAGAGCCCAGAA
GAGGGTGGGCTTCGCAGCGAGCCCTGTGCAGAAATTGCAGGTGCTGCAGTGTCTGAAATTT
CCGGGCTTTTCTAACAGAGGATGTAGCCAGCAACTGTGTCCCGCTCAGTCTTTGAGCGAG
CCCATTTTGTGGATTGTGTCTATGCGCTCATGAGCGTCTGTGGAGCCATCCTCCTGTCTT
AATCGTCCTGCTGCTGCTGCCGTTCCGGTGTGAGCGTCGCCCCGTGACCCTGAGGTGCTCA
ATGATGAGTCCTCTCTGGTCAGACATCGCTGGAATTGAATAGCCAGGCCTGACCTCAAGCAA
CCATGAACCTCAGCTATTAAAGAAAATCACATTTCCAGGGCAGCAGCCGGGATCGATGGTGGCG
CTTTCTCTGTGCCACCCGCTCTTCAATCTCTGTTCTGCTCCAGATGCCTTCTAGATTAC
TGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATCCTCCCTACTTCCAAGAAAAATAATTAA
AAAAAAACTTCATTCTAA

FIGURE 73

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45493

><subunit 1 of 1, 518 aa, 1 stop

><MW: 56180, pI: 5.08, NX(S/T): 2

MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAAATNRVVAPTGPPTPAERHADGLAL
ALEPALASPAGAAANFLAMVDNLQGDSGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTPHS
YIDTYFDTERSSTYRSKGFDTVTKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATIFESNF
FLPGIKWNGILGLAYATLAKPSSSLETFDLSVTQANIPNVFSMQMCGAGLPVAGSGTNGGS
LVLGGIEPSLYKGDIIWYTPIKEEWYQIEILKLEIGGQSLNLDREYNADKAIVDSGTTLLR
LPQKVFDVAVEAVARASLIPEFSDGFWTGSQACWNTSETPWSYFPKISIIYLRDENSRSFR
ITILPQLYIQPMMGAGLNYECYRFGISPTNALVIGATVMEGFYVIFDRAQKRVGFAASPCA
EIAGAAVSEISGPFSTEDVASNCVPAQSLSEPIWIVSYALMSVCGAILLVLLVLLLPFR
QRRPRDPEVVNDESSLVRHRWK

Important features:

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 466-494

N-glycosylation sites.

amino acids 170-173 and 366-369

Leucine zipper pattern.

amino acids 10-31 and 197-118

Eukaryotic and viral aspartyl proteases

amino acids 109-118, 252-261 and 298-310

[illegible]

GCCTCTCCGCTTCGGAGGCTGACGCGCCCGGGCGCCGCTTCCAGGCCCTTGACGGGCGGATGCGAGGCGGCGATGCGAGCCGCTGGCGGCGATCCAGGGCGGTGCGGGGCTGGGCGGGAGCCGGGAGGCGCGGCCGCATGGAGGCGCTGCTGCTGGGCGCGGGGTTGCTGCTGGGCGCTTACGTGCTTGTCTACTACAACTGGTGAAGGCCCCGCGGTGCGGCGGCATGGGCAACCTGCGGGGCGCACGGCCGTGGTACGGGCGCCAACAGCGGCATCGGAAAGATGACGGCGCTGGAGCTGGCGCGCCGGGAGCGCGCGTGGTGTGGCTGCGCGAGCCAGGAGCGCGGGGAGGCGGCTGCCTTCGACCTCCGCCAGGAGAGTGGGAACAATAGAGGTATCTTTCATGGCCTTGGACTTGGCCAGTCTGGCCTCGGTGCGGCTTTGCCACTGCTTTCTGAGCTCTGAGCCACGGTTGGACATCCTCATCCACAATGCCGGTATCAGTTCCTGTGGCCGGACCCGTGAGGCGGTTAAACCTGCTGCTTCGGGTGAACCATACGGTCCCTTTCTGCTGACACATCTGCTGCTGCCTTGCCCTGAAGGCATGTGCCCTTAGCCGCGTGGTGGTGGTAGCCTCAGCTGCCACTGTGCGGGACGCTTGACTTCAAACGCCCTGGAGCCGCCAGTGGTGGGCTGGCGGCAGGAGCTGCGGGCATATGCTGACACTAAGCTGGCTAATGTACTGTTTGCCCGGGAGCTCGCAACCAGCTCTGAGGCCACTGGCGTCACCTGCTATGCAGCCACCAGGGCTGTGAACTCGGAGCTGCTTCTCTCGCCACGAGTTCCTGGATGGCTGCGCCCACTTTTTCGCCCATTTGGCTTGCTGGTGTGTTCCGGGACCAAGAGGGGTGCCCCAGACACCCCTGTATTGTCTCTACAAGAGGGCATCGAGCCCTCAGTGGGAGATATTTTGCCAACTGCCATGTGGAGAGGTGCTGCCCTCAGCTGCCCCGAGACGACCGGGGAGCCCATCGGCTATGGGAGGCGCAGCAAGAGGCTGGCAGGGCTTGGGCTGGGGAGGATGTGTAACCCGATGAAGACCTCCAGTCTGAGGACTAGAGGCCCATCTTCTCTAAGCACCCCCACCCTGAGGAGCCACAGTTTCTCAACCTTACC

CCAGCCCTCAGAGCTACCAGATTGTCTAAGATGACGCACCGAATTACAGGCTAAAGTTGAGCCTGAGATCCAGCTCTCCTAACCCTCAGGCCAGGATGCTTGCCATGGCACTTCATGGTCCTTGAAAACCTCGGATGTGTGTGAGGCCATGCCCTGGACACTGACGGGTTTGTGATCTTGACCTCGTGGTTACTTTCTGGGGCCCCAAGCTGTGCCCTGGACATCTCTTTTCTGGTTGAAGGAATAATGGGTGATTATTTCTTCTCTGAGAGTGACAGTAACCCAGATGGAGAGATAGGGGTATGCTAGACACTGTGCTTCTCGGAAATTGGATGTAGTATTTTCAGGCCCAACCTTATTGATTCTGATCAGCTCTGGAGCAGAGGCGGGAGTTTGCAATGTGATGCACTGCCAACATTGAGAATTAGTGAATGATCCCTTTGCAACCGTCTAGCTAGGTAGTTAAATTACCCCATGTTAATGAAGCGGAATTAGGCTCCCGAGCTAAGGGACTCGCCTAGGGTCTCAGAGTGAGTAGGAGAGGGCCTGGATCTGAACCCAAGGCTCTGAGGCCAGGGCCGACTGCCGTAAGATGGGTGCTGAGAAGTGAGTACGAGCCAGGCAGCTGGTATCAGAGTGCCCATGGGAGTAAGGGGACGCCTTCCGGGCGGTAGCAGGGCTGGGTCTATCTGATCTGAAGCCCTCGGAATAAAGCGGTTGACCGCCAAA

AAAAAAAAAAAAAAAA

FIGURE 75

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48227

<subunit 1 of 1, 377 aa, 1 stop

<MW: 40849, pI: 7.98, NX(S/T): 0

MEALLLGAGLLLGAYVLVYYNLVKAPPCGGMGNLRGRTAVVTGANSIGIGKMTALELARRGAR
VVLACRSQERGEAAAFDLRQESGNNEVIFMALDLASLASVRAFATAFLSSEPRLDILIHNAG
ISSCGRTREAFNLLLRVNHIGPFLTHLLLPCLKACAPSRVVVVASAAHCRGRIDFKRLDRP
VVGWRQELRAYADTKLANVLFARELANQLEATGVTCTAAHPGPVNSELFLRHVPGWLRPLLR
PLAWLVLRAPRGGAQTPLYCALQEGIEPLSGRYFANCHVEEVPPAARDRAAHLWEASKRL
AGLGPGEDAEPDEDQSEDEAPSSLSTPHPEEPTVSQPYPSQSSPDLSKMTTHRIQAKVEP
EIQLS

Important features:

Signal peptide:

amino acids 1-16

Glycosaminoglycan attachment site.

amino acids 46-49

Short-chain alcohol dehydrogenase family

amino acids 37-49 and 114-124

FIGURE 77

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA41404
<subunit 1 of 1, 985 aa, 1 stop
<MW: 105336, pI: 6.55, NX(S/T): 7
MGGMAQDSPPQILVHPQDQLFQGPGPARMSCQASGQPPPTIRWLLNGQLSMVPPDPHLLP
DGTLLLLQPPARGHAHDGQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLREDFQIQPRDM
VAVVGEQFTLECGPPWGHPEPTVSWWKDGKPLALQGRHTVSGGSLLMARAESDEGTYMCV
ATNSAGHRESRAARVSIQEPQDYTEPVELLAVRIQLENTVLLNPDPAEGPKRPAPVWLSWKV
SGPAAPASQSYTALFRTQTAPGGQGAPWAEELLAGWQSABELGGLHWGQDYEFKVRPSSGRARG
PDSNVLLRLPEKVPSAPPQEVTLKPGNGTVFVSWVPPPAENHNGIIRGYQVWSLGNSTSLPP
ANWTVVGEQTQLEIATHMPGSYCVQAAVTGAGAGEPSRPVCLLLEQAMERATQEPSEHGFW
TLEQLRATLKRPEVIATCGVALWLLLLGTAVCIHRRRRARVHLGPGLYRYSSEDAILKHRMD
HSDSQWLADTWRSTSGSRDLSSSSSLSSRLGADARPLDCRRSLLSWDSRSPGVPLLPDTST
FYGSLIAELPSSPTPARPSPQVPAVRRLPPQLAQLSSPCCSSDSLCSRRGLSSPRLSLAPAEA
WKAKKKQELQHANSPLLGRGSHSELRLACELGNRGSKNLSQS PGAVPQALVAVRALGPKLLS
SSNELVTRHLPAPLPFHETPPTQSQQTQPPVAPQAPSSILLPAAPILSPSPSPQASS
LSGPSPASSRLSSSSSLSSLGEDQDSVLTPEEVALCLELSEGEETPRNSVSPMPRAPSPPTY
GYISVPTASEFTDMGRGTGGVGPKGGVLLCPRPCLTPTPSEGLANGWSASEDNAASARA
SLVSSSDGSFLADAHFARALAVAVDSFGFGLEPREADCVPIDASSPPSPRDEIFLTFNLSLP
LWEWRPDWLEDMEVSHQTQRLGRGMPPWPPDSQISSQRSQLHCRMPKAGASFPVDYS
```

Important features:

Transmembrane domain:

amino acids 448-467

N-glycosylation sites:

amino acids 224-227, 338-341, 367-370, 374-377, 658-661 and 926-929

N-myristoylation sites.

amino acids 47-52, 80-85, 88-93, 99-104, 105-110, 181-186, 272-277, 290-295, 355-360, 403-408, 462-467, 561-566, 652-657, 849-854 and 876-881

Phosphotyrosine interaction domain proteins

amino acids 740-753

FIGURE 78

CTCCCACGGTGTCCAGCGCCAGAAATGCGGCTTCTGGTCTGCTATGGGGTTGCCCTGCTGCT
 CCCAGGTTATGAAGCCCTGGAGGGCCAGAGGAAATCAGCGGGTTTGAAGGGGACACTGTGT
 CCCTGCAGTGCACCTACAGGGAAGAGCTGAGGGACACCAGGAAGTACTGGTGCAGGAAGGGT
 GGGATCCTCTTCTCGTCTGCTCTGGCACCATCTATGCAGAAAGAAAGGCCAGGACCAAT
 GAAGGGCAGGGTGTCCATCCGTGACAGCCGCCAGGAGCTCTCGCTCATTTGTGACCCCTGTGGA
 ACCTCACCCCTGCAAGACGCTGGGGAGTACTGGTGTGGGGTCGAAAAACGGGGCCCGATGAG
 TCTTTACTGATCTCTCTGTTGCTCTTCCAGGACCTGTGTCTCTCCCTCCCTCTTCCAC
 CTTCCAGCCTCTGGCTACAACACGCTGCAGCCAAAGGCAAAAGCTCAGCAAAACCCAGCCCC
 CAGGATTGACTTCTCTGGGCTTACCCGGCAGCCACCACAGCCAAGCAGGGGAAGACAGGG
 GCTGAGGCCCCCTCCATTGCCAGGGACTTCCAGTACGGGCACGAAAGGACTTCTCAGTACAC
 AGGAACCTCTCCTCACCCAGCGACCTCTCCTCCTGCAGGGAGCTCCCCCCCCCCTATGCAGC
 TGGACTCCACCTCAGCAGAGGACACAGTCCAGCTCTCAGCAGTGGCAGCTCTAAGCCCAAG
 GTGTCCATCCCGATGTTCCGCATACTGGCCCCAGTCTGTGTGCTGCTGAGCCTTCTGTGAGC
 CGCAGGCTGTATGCTCTTCTGCAGCCACTGCTCCTGTGGAGAAAGGAAGCTCAACAGGGCCA
 CGGAGACACAGAGGAACGAGAAGTTCTGGCTCTCAGCGTTGACTGCGGAGGAAAGGAGGCC
 CCTTCCCAGGCCCTGAGGGGGACGTGATCTCGATGCCTCCCCTCCACACATCTGAGGAGGA
 GCTGGGCTTCTCGAAGTTTGCTCTCAGCGTGGGCGAGGAGGCCCTCTGGCCAGGCCAGCAGT
 GAAGCAGTATGGCTGTGGATCAGCACCGATTCCCGAAAGCTTTCCACCTCAGCCTCAGAG
 TCCAGCTGCCCGGACTCCAGGGCTCTCCCCACCTCCACAGGCTCTCCTCTTGCATGTTTCA
 GCCTTGACCTAGAACGCTTTGCTCAGCCCTGGAGCCACAGCGGTGGCCTTGCTCTTCCGGCTG
 GAGACTGGGACATCCCTGATAGGTTACATCCCTGGGCAGAGTACACAGGCTGTGACCCCTCA
 GCAGGGCCAGACAAGGCTCAGTGGATCTGGTCTGAGTTTCAATCTGCCAGGAACCTCTGGGC
 CTCATGCCCAGTGTGGACCTGCCTTCTCCCACTCCAGACCCACCTTGCTTCTCCCTCCC
 TGGCGTCTCAGACTTAGTCCCACGGTCTCCTGCATCAGCTGGTGATGAAGAGGAGCATGCT
 GGGGTGAGACTGGGATTCTGGCTTCTCTTTGAACCACCTGCATCCAGCCCTTCAGGAAGCCT
 GTGAAAAACGCTGATTCTCTGGCCCCACCAAGACCCACCAAAACCATCTCTGGCCTTGGTGAG
 GACTCTGAATTTAAACAATGCCCAGTGAAGTGTGCACTTGAGTTTGAAGGCCAGTGGGCCGTG
 ATGAACGCTCACACCCCTTACGCTTAGAGTTGAGTCTGCAATTTGGGCTGTGAGCTCTCCACTGCC
 CAATAGATCTGCTCTGCTCTGCGACACCAGATCCACGTGGGGACTCCCTTGAGGCCCTGCTAAG
 TCCAGGCCCTTGGTCAGGTCAAGTGCAATTGCAGGATAAGCCAGGACCGGCACAGAAGTGG
 TTGCCCTTNCATTGTCCTCCTGGNCCATGCCCTTCTTGCCCTTGGAAAAATGATGAAGA
 AAACCTTGGCTCCTTCTTCTGTGGAAAGGGTTACTTGCTATGGGTTCTGGTGGCTAGAGA
 GAAAAAGTAGAAAAACCAAGTGCACGTAGGTGTCTAACACAGAGGAGAGTAGGAACAGGGCGG
 ATACCTGAAGGTGACTCCGAGTCCAGCCCCGTGGAGAAGGGGTGGGGGTGGTGTAAAGTA
 GCACAACTACTATTTTTTTCTTTTTCCATTATTATTTGTTTTTAAAGACAGAACTCTCGTGT
 GCTGCCCAGGCTGGAGTGCAGTGGCACGATCTGCAAACTCCGCTCTCGGCTTCAAGTGATT
 CTTCTGCCTCAGCCTCCGAGTAGCTGGGATTACAGGCACGCCACCACACCTGGCTAATT
 TTTGTACTTTTAGTAGAGATGGGGTTTACCATTGTTGGCCAGGCTGTGCTTTGAACCTCTGAC
 CTCAAAATGAGCCTCTGCTTCACTCAGTCTCCAAATGCGGGGATTACAGGCATGAGCCACTGTG
 TCTGGCCCTATTCTCTTTAAAGTGAAATTAAGAGTTGTTTCAAGTATGCAAACTTTGGAAG
 ATGAGGAGAAAAAGAAAGGAAGAAAAATGTACCCCATAGTCTCACCAGAGACTATCAT
 TATTTCTGTTTTGTTGTAAGTCTTCTTCCACTTTTCTTCCATAATTTGCCGGTGTCTT
 TTTACAGAGCAATTTATCTGTATATACAACCTTTGTATCCTGCCTTTTCCACCTTATCGTTCC
 ATCACTTTATTCAGCACTTCTGTGTTTTACAGACCTTTTTATAAATAAAATGTTTCATCA
 GCTGCATAAAAAAAAAAAAAA

FIGURE 79

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44196

<subunit 1 of 1, 332 aa, 1 stop

<MW: 36143, pI: 5.89, NX(S/T): 1

MRLLVLLWGCLLLPGYEALGPEEISGFEGDTVSLQCTYREELRDHRKYWCRKGGILFSRCS
GTIYAEEEGQETMKGRVSIRDSRQELSLIVTLWNLTLDAGEYWCVGVEKRGPDSELLISLFV
FPGPCCPPSPSPTFQPLATTRLQPKAKAQQTQPPGLTSPGLYPAATTAKQGKTGAEEAPPLPG
TSQYGHERTSQYTGTSHPHPATSPAGSSRPPMQLDSTSAEDTSPALSSGSSKPRVSIPMVRI
LAPVLVLLSLLSAAGLIAFCSHLLLWRKEAQQATETQRNEKFWLSRLTAAEEKEAPSAPEGD
VISMPPLHTSEELGFSKFVSA

Important features:

Signal peptide:

amino acids 1-17

Transmembrane domain:

amino acids 248-269

N-glycosylation site.

amino acids 96-99

Fibrinogen beta and gamma chains C-terminal domain.

amino acids 104-113

Ig like V-type domain:

amino acids 13-128

FIGURE 80

TTGTGACTAAAAGCTGGCCTAGCAGGCCAGGGAGTGCAGCTGCAGGCGTGGGGGTGGCAGGA
GCCGCAGAGCCAGAGCAGACAGCCGAGAAACAGGTGGACAGTGTGAAAGAACCAGTGGTCTC
GCTCTGTTGCCCAGGCTAGAGTGTACTGGCGTGATCATAGCTCACTGCAGCCTCAGACTCCT
GGACTTGAGAAAATCCTCCTGCCTTAGCCTCCTGCATATCTGGGACTCCAGGGGTGCACTCAA
GCCCTGTTTCTTCTCCTTCTGTGAGTGGACACGGAGGCTGGTGAGCTGCCTGTCTATCCCAA
AGCTCAGCTCTGAGCCAGAGTGGTGGTGGCTCCACCTCTGCCGCCGGCATAGAAGCCAGGAG
CAGGGCTCTCAGAAGGCGGTGGTGCCAGCTGGGATCATGTTGTTGGCCCTGGTCTGTCTGC
TCAGCTGCCTGCTACCTCCAGTGAGGCCAAGCTCTACGGTCGTTGTGAACTGGCCAGAGTG
CTACATGACTTCGGGCTGGACGGATACCGGGGATACAGCCTGGCTGACTGGGTCTGCCTTGC
TTATTTTCAACAAGCGGTTTCAACGCAGCTGCTTTGGACTACGAGGCTGATGGGAGCACCAACA
ACGGGATCTTCCAGATCAACAGCCGGAGGTGGTGCAGCAACCTCACCCGAACGTCCCCAAC
GTGTGCCGGATGTACTGCTCAGATTTGTTGAATCCTAATCTCAAGGATACCGTTATCTGTGC
CATGAAGATAACCCAAGAGCCTCAGGGTCTGGGTACTGGGAGGCCTGGAGGCATCACTGCC
AGGGAAAAGACCTCACTGAATGGGTGGATGGCTGTGACTTCTTAGGATGGACGGAACCATGCA
CAGCAGGCTGGGAAATGTGGTTTGGTTCTTGACCTAGGCTTGGGAAGACAAGCCAGCGAATA
AAGGATGGTTGAACGTGAAA

FIGURE 81

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52187

<subunit 1 of 1, 146 aa, 1 stop

<MW: 16430, pI: 5.05, NX(S/T): 1

MLLALVCLLSCLLPSEAKLYGRCELARVLHDFGLDGYRGYSLADWVCLAYFTSGFNAAALD
YEADGSTNNGIFQINSRRWCSNLTENVPNVCRMYCSDLLNPNLKDTVICAMKITQEPQGLGY
WEAWRHHCQGKDLTEWVDGCDF

Important features:

Signal peptide:

amino acids 1-18

N-myristoylation site.

amino acids 67-72

Homologous region to Alpha-lactalbumin / lysozyme C proteins.

amino acids 34-58 (catalytic domain), 111-132 and 66-107

FIGURE 82

AGCCGCTGCCCCGGGCGGGCGCCGCGGCGGCACCATGAGTCCCCGCTCGTGCCCTGCGTTT
GCTGCGCCTCCTCGTCTTCGCGCTCTTCTCAGCCGCGCGAGCAACTGGCTGTACCTGGCCA
AGCTGTCGTCGGTGGGAGCATCTCAGAGGAGGACGTGCGAGAACTCAAGGGCCTGATC
CAGAGGCAGGTGCAGATGTGCAAGCGGAACCTGGAAGTCACTGGACTCGGTGCGCCGCGGTGC
CCAGCTGGCCATTGAGGAGTGCCAGTACCAGTTCCGGAACCGGCGCTGGAACCTGCCACAC
TCGACTCCTTGCCCGTCTTCGGCAAGGTGGTGACGCAAGGAACTCGGGAGGCGGCTTCGTG
TACGCCATCTCTTCGGCAGGTGTGGCCTTTGCAGTGACGCGGCGTGACAGCTGGGGAGCT
GGAGAAGTGCGGCTGTGACAGGACAGTGCATGGGGTCAGCCACAGGGCTTCCAGTGGTCAG
GATGCTCTGACAAATCGCCTACGGTGTGGCCTTCTCACAGTCGTTTGTGGATGTGCGGGAG
AGAAGCAAGGGGGCCTCGTCCAGCAGAGCCCTCATGAACCTCCACAACATGAGGCCGGCAG
GAAGCCATCTGACACACATGCGGGTGAATGCAAGTGCCACGGGGTGTGAGGCTCCTGTG
AGGTAAAGACGTGCTGGCGAGCCGTGCCGCCCTTCCGCCAGGTGGGTACGCACTGAAGGAG
AAGTTTGATGGTGCCACTGAGGTGGAGCCACGCCGCGTGGGCTCCTCCAGGGCACTGGTACC
ACGCAACGCACAGTTCAAGCCGCACACAGATGAGGACCTGGTGTACTTGAGGCTAGCCCCG
ACTTCTGTGAGCAGGACATGCGCAGCGCGTGTGTTGGGCAGAGGGGCCGCACATGCAACAAG
ACGTCCAAGGCCATCGACGGCTGTGAGCTGTGTGCTGTGGCCGCGGCTTCCACACGGCGCA
GGTGGAGCTGGCTGAACGCTGCAGCTGCAAAATCCACTGGTGTGCTTCGTCAAGTGCCGGC
AGTGCCAGCGGCTCGTGGAGTTGCACACGTGCCGATGACCGCTGCTAGCCCTGCGCCGGC
AACCACCTAGTGGCCAGGGAAGGCCGATAATTTAAACAGTCTCCACCACCTACCCCAAGA
GATACTGGTTGTATTTTTTTTCTGTTCTGGTTTGGGTCTCATGTTATTTATTGCGGAA
ACCAGGCAGGCAACCCCAAGGGCACCAACCAGGGCTCCCCAAAGCCTGGGCCCTTGTGGCT
GCCACTGACCAAAGGACCTTGCTCGTGCCGCTGGCTGCCCGCATGTGGCTGCCACTGACCA
CTCAGTTGTTATCTGTGTCGTTTCTACTTGACAGACCTAAGGTGGAGTAACAAGGAGTAT
TACCACCACATGGCTACTGACCGTGTATCGGGGAAGAGGGGCTTATGGCAGGAAAAATA
GGTACCGACTTGATGGAAGTACACCCCTTGGAAGAAAGAACTCTTAACCTCCAGCACACA
TACACATGGACTCTGGCAGCTTGAGCCTAGAAGCCATGTCTCTCAAATGCCCTGAGAAAGG
GAACAAGCAGATACAGGTCAAGGGCACCAGGTTCAATTCAGCCCTTACATGGACAGCTAGA
GGTTGCATATCTGTGGGTCTTCCAGGCAAGAAGAGGAGATGAGAGCAAGAGACGACTGAA
GTCCACCCCTAGAACCAGCCTGCCCCAGCCTGCCCTGGGAAGAGGAACTTAACCACTCC
CCAGACCCACCTAGGCAGGCATATAGGCTGCCATCCTGGACCAGGGATCCCGGCTGTGCCTT
TGCAGTCATGCCGAGTCACCTTTCACAGCGCTGTCTCCTCATGAAACTGAAAAACACACAC
ACCTGCGAGA
GAGAGGGAGGAAAGGCTGTGCCTTTGCAGTCATGCCGAGTCACCTTTCACAGCACTGTTCTCT

FIGURE 83

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48328

<subunit 1 of 1, 351 aa, 1 stop

<MW: 39052, pI: 8.97, NX(S/T): 2

MSPRSCLSRLRLLVFAVFSAAAASNWLYLAKLSSVGSISEEETCEKLKGLIQRQVQMCKRNLE
VMDSVRRGAQLAIEECQYQFFNRNRWNCSTLDSLVPVFGKVVTQGTREAAAFVYAISSAGVAFV
TRACSSGELEKCGCDRTVHGVSPQGFQWSGCSDNIAYGVAFSQSFVDVRERSKGASSSRALM
NLHNNEAGRKAILTHMRVECKCHGVSGSCEVKTWRAVPPFRQVGHALKEKFDGATEVEPRR
VGSSRALVPRNAQFKPHTDEDLVYLEPSPDFCEQDMRSGVLGTRGRTCNKTSKAIDGCELLC
CGRGFHTAQVELAERCCKFWCCFVKCRQCQRLVELHTCR

Important features:

Signal peptide:

amino acids 1-22

N-glycosylation sites.

amino acids 88-91 and 297-300

Wnt-1 family signature.

amino acids 206-215

Homologous region to Wnt-1 family proteins

amino acids 183-235, 305-350, 97-138, 53-92 and 150 -174

FIGURE 84

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCTGGGTGCCTGCAT
CGCCATATGGACACCACCAGGTACAGCAAGTGGGGCGGCAGCTCCGAGGAGGTCCCCGAGGGGC
CCTGGGGACGCTGGGTGCACTGGAGCAGGAGACCCCTCTTCTTGGCCCTGGCTGTCTGGTTC
ACCACAGTCTCTTTGGGCTGTGATTCTGAGTATCCTATTGTCCAAGGCTCCACGGAGCGCGC
GGCGCTGCTTGACGGCCACGACCTGCTGAGGACAAACGCCTCGAAGCAGACGGCGCGCTGG
GTGCCCTGAAGGAGGAGGTTCGGAGACTGCCACAGCTGCTGCTCGGGGACGCAGGCGCAGCTG
CAGACCACGCGCGCGGAGCTTGGGGAGGCGCAGGCGAAGCTGATGGAGCAGGAGAGCGCCCT
GCGGGAACTGCGTGAGCGCGTGACCCAGGGCTTGGCTGAAGCCGCGCAGGGGCCGTGAGGACG
TCCGCACTGAGCTGTTCCGGGCGCTGGAGGCCGTGAGGCTCCAGAACTCCTGCGAGCCG
TGCCCCACGTCTGTGGCTGTCTTTCGAGGGCTCCTGCTACTTTTTCTCTGTGCCAAAGACGAC
GTGGGCGGCGGCGCAGGATCACTGCGCAGATGCCAGCGCGCACCTGGTGATCGTTGGGGGCC
TGGATGAGCAGGGCTTCTCACTCGGAACACGCGTGGCCGTGGTTACTGGCTGGGCCTGAGG
GCTGTGCGCCATCTGGGCAAGGTTTCAGGGCTACCACTGGGTGGACGGAGTCTCTCTCAGCTT
CAGCCACTGGAACACAGGGAGAGCCCAATGACGCTTGGGGGCGCGAGAAGTGTGTATGATGC
TGACACGCGGGGCTGTGGAAACGACGACCGTGTGACAGCGAGAAGGACGGCTGGATCTGTGAG
AAAAGGCACAACCTGCTTGACCCCGCCCAGTGCCCTGGAGCCGCGCCCATTCGAGCATGTCTGTA
TCCTGGGGGCTGCTCACCTCCCTGGCTCCTGGAGCTGATTGCCAAAGAGTTTTTTTCTTCTCT
CATCCACCGCTGCTGAGTCTCAGAAACACTTGGCCCAACATAGCCCTGTCCAGCCCACTGCCC
TGGGCTCTGGGACCTCCATGCCACCTCATCTAACTCCACTCACGCAGACCAACCTAACC
TCCACTAGCTCCAAAAATCCCTGCTCCTTGCGTCCCCTGATATGCCTCCACTTCTCTCCCTAA
CCAAGGTTAGGTGACTGAGGACTGGAGCTGTTTGGTTTTCTCGCATTTTCCACCAAACCTGGA
AGCTGTTTTTGCAGCCTGAGGAAGCATCAATAAATATTGAGAAATGAAAAA

FIGURE 85

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56352

<subunit 1 of 1, 293 aa, 1 stop

<MW: 32562, pI: 6.53, NX(S/T): 2

MDTTRYSKWGGSSSEVPGGPWGRWVHWSRRPLFLALAVLVTTVLWAVILSILLSKASTERAA
LLDGHDLLRTNASKQTAALGALKEEVGDCHSCCSGTQAQLQTTRAELEGQAQAKLMEQESALR
ELRERVTOGLAEAGRGREDEVTELFRALAVRLQNNSCPECPPTSWLSFEGSCYFFSVPKTTW
AAQDHCADASAHLVIVGGLEDEQGFLTRNTRGRGYWLGLRAVRHLGKVQGYQWVDGVSLSFS
HWNQGEPNDAWGRENCVMMLHTGLWNDAPCDSEKDGWICEKRHNC

Important features:

Type II transmembrane domain:

amino acids 31-54

N-glycosylation sites.

amino acids 73-76 and 159-162

Leucine zipper pattern.

amino acids 102-123

N-myristoylation sites.

amino acids 18-23, 133-138 and 242-247

C-type lectin domain signature.

amino acids 264-287

FIGURE 86

GCCAGGGGAAGAGGGTGATCCGACCCGGGGAAGGTCGCTGGGCAGGGCGAGTTGGGAAAGCG
GCAGCCCCCGCCGCCCGCGAGCCCTTCTCCTCTTCTCCACGTCTATCTGCCTCTCG
CTGGAGGCGAGGCGGTGCAGCATCGAAGACAGGAGGAACCTGGAGCCTCATTGGCCGGCCCGG
GGCGCCGGCCTCGGGCTTAAATAGGAGCTCCGGGCTCTGGCTGGGACCCGACCGCTGCCCGC
CGCGCTCCCGTGTCTCTGCGGGTGATCGAATAACCCAGCCCGCCCGCCCTGGGCAAG
GCCCTCTGCGCTCTCCTCTGGCCACTCTCGGCGCCCGGCCAGCCTCTTGGGGGAGAGTC
CATCTGTTCCGCCAGAGCCCCGGCCAAATACAGCATCACCTTCAGGGCAAGTGGAGCCAGA
CGGCCTTCCCAAAGCAGTACCCCCCTGTTCCGCCCCCTGCGCAGTGGTCTTTCGTGCTGGGG
GCCGCGCATAGCTCCGACTACAGCATGTGGAGGAAGAACCAGTACGTAGTAACGGGCTGCG
CGACTTTGCGGAGCGCGCGAGGCTGGGCGCTGATGAAGGAGATCGAGGCGCGGGGGAGG
CGCTGCAGAGCGTGCACGAGGTGTTTTCGGCGCCCGCGTCCCGAGCGCACCGGGCAGACG
TCGGCGGAGCTGGAGGTGCAGCGCAGGCACTCGCTGGTCTCGTTTGTGGTGCGCATCGTCC
CAGCCCCGACTGGTTCTGTGGGCGTGGACAGCCTGGACCTGTGCGACGCGGGACCGTGTGGCGG
AACAGGCGGCGTGGACCTGTACCCCTACGACGCGGGACGGACAGCGGCTTCACCTTCTCC
TCCCCCAACTTCGCCACCATCCCGCAGGACACGGTGACCGAGATAACGTCTCTCTCCAG
CCACCCGGCCAACTCCTTCTACTACCCGCGGTGAAGGCCCTGCTCCCATCGCCAGGGTGA
CACTGCTGCGGCTGCGACAGAGCCCCAGGCTTCATCCTCCCGCCCCAGTCTGCCCAGC
AGGGACAATGAGATTGTAGACAGCGCCTCAGTTCCAGAAACGCCGCTGGACTGCGAGGTCTC
CCTGTGGTGTCTCTGGGGACTGTGCGGAGGCCACTGTGGGAGGCTCGGGACCAAGAGCAGGA
CTCGCTACGTCCGGGTCCAGCCCCCAACAACGGGAGCCCTGCCCGAGCTCGAAGAAGAG
GCTGAGTGCCTCCCTGATAAATGCGCTCTAAGACCAGAGCCCCGAGCCCTGGGGCCCCCG
GAGCCATGGGGTGTGGGGGCTCCTGTGCAGGCTCATGCTGCAGGCGGCGGAGGGCACAGGG
GGTTTCGCGCTGTCTCTGACCGCGGTGAGGCGCGCGGACCATCTCTGCACTGAAGGGCCCT
CTGGTGGCGGCGACGGGCATTGGGAAACAGCCTCCTCTTTCCCAACCTTGCTTCTTAGGGG
CCCCGTGTCCCGTGTCTCTCAGCCTCCTCCTCTGCAGGATAAAGTCATCCCCAAGGCTC
CAGCTACTCTAAATATGTCTCCTTATAAGTTATTGCTGCTCCAGGAGATTGCTCTTCATCG
TCCAGGGGCTTGGCTCCCAGTGGTTGCAGATACCTCAGACCTGGTGTCTAGGCTGTGCTG
AGCCCACTCTCCCGAGGCGCATCCAAGCGGGGCCACTTGAGAAGTGAATAAATGGGGCGG
TTTCGGAAGCGTCAGTGTTCATGTATGGATCTCTGCGTTTGAATAAGACTATCTCT
GTTGCTCACAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 87

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53971

><subunit 1 of 1, 331 aa, 1 stop

><MW: 35844, pI: 5.45, NX(S/T): 2

MENPSPAAALGKALCALLLATLGAAGQPLGGESIC SARAPAKYSITFTGKWSQTAFPKQYPL
FRPPAQWSSLLGAAHSSDYSMWRKNQYVVSNGLRDFAERGEAWALMKEIEAAGEALQSVHEVF
SAPAVPSGTGQTSAELEVQRRHSLVSFVVRIVPSPDWFVGVDSLDLCDGDRWREQAALDLYP
YDAGTDSGFTFSSPNFATIPQDTVTEITSSSPSHPANSFYYPRLKALPPIARVTLLRLRQSP
RAFIPPPAPVLPSRDNEIVDSASVPETPLDCEVSLWSSWGLCGGHCGRLGTKSRTRYVRVQPA
NNGSPCPELEEEAECPDNCV

Important features:

Signal peptide:

amino acids 1-26

Figure 1

(a) H_2O molecule

 Oxygen atom (center)
 Hydrogen atoms (left and right)

(b) H_2O molecule

 Oxygen atom (center)
 Hydrogen atoms (left and right)

(c) H_2O molecule

(d) H_2O molecule

(e) H_2O molecule

(f) H_2O molecule

(g) H_2O molecule

(h) H_2O molecule

(i) H_2O molecule

(j) H_2O molecule

(k) H_2O molecule

(l) H_2O molecule

(m) H_2O molecule

(n) H_2O molecule

(o) H_2O molecule

(p) H_2O molecule

(q) H_2O molecule

(r) H_2O molecule

(s) H_2O molecule

(t) H_2O molecule

(u) H_2O molecule

(v) H_2O molecule

(w) H_2O molecule

(x) H_2O molecule

(y) H_2O molecule

(z) H_2O molecule

GGCGCGCTCCGTGAGGGGCTCCTTTGGCAGGGGTAGTGGTTGGTGTCCTTGCTCTTGCGTGA
TATTGACAAACTGAAGCTTTCTTGCACCACTGGACTTAAGGAAGAGTGTA CTCTG TAGGCGGA
CAGCTTTAGTGGCCGGCCGGCCGCTCTCATCCCCGTAAAGGAGCAGAGTCCTTTGTACTGAC
CAAGATGAGCAACATCTACATCCAGGAGCCTCCACGAATGGGAAGGTTTTATTGAAAACTA
CAGCTGGAGATATTGACATAGAGTTGTGGTCCAAGAAGCTCCTAAAGCTTG CAGAAATTTT
ATCCAACCTTTGTTTGGAAAGCTTATTATGACAATACCATTTTTCATAGAGTTGTGCCTGGTTT
CATAGTCCAAGGCGGAGATCCTACTGGCA CAGGAGTGTTGGAGAGTCTATCTATGGAGCGC
CATTCAAAGATGAATTTCA TTCACGGTTGCGTTTTAATCGGAGAGGACTGGTTGCCATGGCA
AATGCTGGTTCTCATGATAATGGCAGCCAGTTTTTCTTCACTGGGTCGAGCAGATGAACT
TAACAATAAGCATACCATCTTTGGAAGGTTACAGGGGATACAGTATATAACATGTTGCGAC
TGT CAGAAGTAGACATTGATGATGACGAAAGACCATAAATCCACACAAAATAAAAAGCTGT
GAGGTTTTGTTTAACTCTTTTGATGACATCATTCCAAGGGAATTAAGAGCTGAAAAAGA
GAAACCGACAGGAGGAAGTAAAGAAATTGAAACCCAAAGGCACAAAAAATTTAGTTTACTTT
CATTTGGAGAGGAAGCTGAGGAAGAAGAGGAGGAAGTAATCGAGTTAGTCAGAGCATGAAG
GGCAAAAGCAAAAGTAGTCACTAGCTTGTCTTAAGGATGATCCACATCTGCTTCTGTTCCAGT
TG TAGAAAGTGA AAAAGGTGATGCACCAGATTTAGTTGATGATGGAGAAGATGAAAGTCGAG
AGCATGATGAATATATTGATGGTGATGAAAAGAACTGATGAGAGAAAGAAATGCCAAAAA
TTAAAAAAGGACACAAGTCGAATGTTAAATCAGCTGGAGAGTGAAGTGGAGAAGAAATC
AGTCAGCCG CAGTGAAGAGCTCAGAAAAGAAGCAAGACAATTAACACGGGAACCTTTAGCAG
CAAAACAAAAAAGTAGAAAATGCAGCAAAACAAGCAGAAAAAAGAAGTGAAGAGGAAGAA
GCCCCCTCCAGATGGTGCTGTTGCCGAATACAGAAGAGAAAAGCAAAAGTATGAAGCTTTGAG
GAAGCAACAGTCAAAGAGGGGAACCTTCCGGGAAGATCAGACCCCTGCACTGCTGAACCACT
TTAAATCTAAACTCACTCAAGCAATTGCTGAAACACCTGAAAATGACATTCCTGAAACAGAA
GTAGAAGATGATGAAGGATGGATGTCCATGTACTTCAGTTT GAGGATAAAAGCAGAAAAGT
GAAAGATGCAAGCATGCAAGACTCAGATACATTTGAAATCTATGATCCTCGGAATCCAGTGA
ATAAAAGAAGGAGGGAAGAAAGCAAAAAGCTGATGAGAGAGAAAAAGAAAGAAGATAAAT
GAGAATAATGATAAC CAGA ACTTGCTGGAATGTGCC TACAATGGCCTTGTAA CAGCCATTG
TTCCCAACAGCATCACTTAGGGGTGTGAAAAGAAGTATTTTTGAACCTGTTGTCTGGTTTTG
AAAAACAATTATCTGTTTGTGCAAAATGTGGAATGTGTAAGCAAATGCCTTTTGGTTACTGG
TACATGTGTTTTTCTTCTAGCTGACCTTTTATATGTCTAAATCTGAAATAAAATAACTTTCCT
TCCACAAAAA AAAAAAAAAAAAAAAAAAAAAA

FIGURE 89

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50919
><subunit 1 of 1, 472 aa, 1 stop
><MW: 53847, pI: 5.75, NX(S/T): 2
MSNIYIQEPPTNGKVLKTTAGDIDIELWSKEAPKACRNFIQLCLEAYDNTIFHRVVPGFI
VQGGDPTGTGSGGESIYGAPFKDEFHSLRFRNRRGLVAMANAGSHDNGSQFFFTLGRADELN
NKHTIFGKVTGDTVYNMLRLSEVDIDDDERPHNPHKIKSCEVLFNPFDDIIIPREIKRLKKEK
PEEEVKLKPCKGTKNFSLLSFGEEAEEEEEEVNRVSQSMKGKSKSSHDLKDDPHLSSVPVV
ESEKGDAPDLVDDGEDESAEHDEYIDGDEKNLMRERIACKLKKDTSANVKSAGEGEVEKKSV
SRSEELRKEARQLKRELLAAKQKKVENAAKQAEKRSEEEAAPPDGAVAEYRREKQKYEALRK
QQSKKGTSREDQTLALLNQPKSKLTQAIAETPENDIPETEVEDDEGWMSHVLQFEDKSRKVK
DASMQSDSTFEIYDPRNPVNKRREESKCLMREKKERR

Important features:

Signal peptide:

amino acids 1-21

N-glycosylation sites.

amino acids 109-112 and 201-204

Cyclophilin-type peptidyl-prolyl cis-trans isomerase signature.

amino acids 49-66

Homologous region to Cyclophilin-type peptidyl-prolyl cis-trans isomerase

amino acids 96-140, 49-89 and 22-51

FIGURE 91

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44179

<subunit 1 of 1, 545 aa, 1 stop

<MW: 58934, pI: 9.45, NX(S/T): 4

MSTGFSFGSGTLGSTTTVAAGGTSTGGVFSFGTGTSSNPSVGLNFGNLGSTSTPATTSAPSSG
FGTGLFGSKPATGFTTLGGTNTGALHTKRPQVVTKYGTLLQGKQMHVGKTPIQVFLGVFFSRPP
LGILRFAPPEPPEPWKGIRDATTYPGWSLALSPGWSAVARSRLTATSASRVQASLLPQPLS
VWGYRCLQESWGLASMYVSTRERYKWLRFSEDCLYLNVYAPARAPGDPQLPVMVWFPGGAF
IVGAASSYEGSDLAAREKVVVLVFLQHRLGIFGFLSTDDSHARGNWGLLDQMAALRWVQENIA
AFGGDPGNVTLFGQSAGAMISGLMMSPLASGLFHRAISQSGTALFRLFITSNPLKVAKKVA
HLAGCNHNSTQILVNCLRALSGTKVMRVSNMKMRFLQLNFQRPDEEIIWSMSPVVDGVVIPDD
PLVLLTQGVSSVPYLLGVNNLEFNWLLPYNITKEQVPLVVEEYLDNVNEHDWKMLRNRMMMD
IVQDATFVYATLQTAHYHRETMMGICPAGHATTRMKSTCSWILPQEWA

Important features:

Signal peptide:

amino acids 1-29

Carboxylesterases type-B serine active site.

amino acids 312-327

Carboxylesterases type-B signature 2.

amino acids 218-228

N-glycosylation sites.

amino acids 318-321, 380-383 and 465-468

FIGURE 92

GAGAACAGGCCTGTCTCAGGCAGGCCCTGCGCCTCCTATGCGGAGATGCTACTGCCACTGTCT
GCTGTCTCTCGTCTCTGGGCGGGTCCCAGGCTATGGATGGGAGATTCTGGATACGAGTGCAGG
AGTCAGTGAATGGTGCCGAGGGCCCTGTGCATCTCTGTGCCCTGCTCTTTCTCTCTACCCCCGA
CAAGACTGGACAGGGTCTACCCAGCTTATGGCTACTGGTTCAAAGCAGTGACTGAGACAAC
CAAGGGTGTCTGTGTGCCACAAACCACCAGAGTCGAGAGGTGGAAATGAGCACCCTGGGGCC
GATTCCAGCTCACTGGGGATCCCGCCAAAGGGGAAGTCTCTCTGGTGATCAGAGACGCGCAG
ATGCAGGATGAGTCACAGTACTTCTTTGGGTGGAGAGAGGAAGCTATGTGACATAATAATT
CATGAACGATGGGTTCTTTCTAAAGTAACAGTGCTCAGCTTACGCCCCAGACCCAGGACC
ACAACACCGACTCACCTGCCATGTGGACTTCTCCAGAAAGGGTGTGAGCGCACAGAGGACC
GTCCGACTCCGTGTGGCTATGCCCCAGAGACCTTGTATCAGCATTTCAGTGCACAACAC
GCCAGCCCTGGAGCCCCAGCCCCAGGGAAATGTCCATACCTTGAAGCCCAAAAGGCCAGT
TCCTGCGGCTCTCTGTGCTGCTGACAGCCAGCCCCCTGCCACACTGAGCTGGTCTGTGCAG
AACAGAGTCTCTCTCTGTCCATCCCTGGGGCCCTAGACCCCTGGGGCTGGAGCTGCCCGG
GGTGAAGGCTGGGATTCAGGGCGCTACACCTGCCGAGCGGAGAGCTTGGCTTGGCTCCAGC
AGCGAGCCCTGGACCTCTCTGTGCAGTATCCTCCAGAGAACCTGAGAGTGATGGGTTTCCAA
GCAAAACAGGACAGTCTGTGAAACCTTGGGAACGGCACGTCTCTCCAGTACTGGAGGGCCA
AAGCCTGTGCTGGTCTGTGTACACACAGCAGCCCCCAGCCAGGCTGAGCTGGACCCAGA
GGGACAGGTTCTGAGCCCTCCCAGCCCTCAGACCCCGGGGCTCTGGAGCTGCTCCTGGGTT
CAAGTGGAGCAGAAGGAGAGTTCACCTGCCACGCTCGGCACCACTGGGCTCCAGCAGCT
CTCTCTCAGCCTCTCCGTGCACTATAAGAAGGAGTCACTCAACGGCATTCTCAACGGAG
CGTTTCTGGGAATCGGCATCACGGCTCTTCTTTTCTCTGCTGCGCTGGCCCTGATCATGAAG
ATTCTACCGAAGAGACGGACTCAGACAGAAACCCGAGGCCCAGGTTCTCCGGGCACAGCAC
GATCCTGGATTACATCAATGTGGTCCCGACGGCTGGCCCCCTGGCTCAGAAGCGGAATCAGA
AAGCCACACCAACAGTCTCTCGGACCCCTCTCCACCAAGGTGCTCCCTCCCGAGAATCAAG
AAGAACCAGAAAAAGCAGTATCAGTTGCCAGTTCCTCCAGAACCCAAATCATCCACTCAAGC
CCCAGAATCCCAGGAGAGCCAAGAGGAGTCCATTATGCCACGCTCAACTCCAGGCGTCA
GACCCAGGCCCTGAGGCCCGGATGCCCAAGGGCACCAGGCGGATTATGCAGAAGTCAAGTTC
CAATGAGGGTCTCTTAGGCTTTAGGACTGGGACTCGGCTAGGGAGGAAGGTAGAGTAAGAG
GTTGAAGATAACAGAGTGCAAAAGTTTCTTCTCTCCCTCTCTCTCTCTCTCTCTCTCTCT
CTCTCTTCTCTCTCTTTTAAAAAACATCTGGCCAGGGCACAGTGGCTCACGCCCTGTAATC
CCAGCACTTTGGGAGGTTGAGGTGGGCAGATCGCCTGAGGTGGGAGTTTCGAGACCAGCCTG
GCCAATTTGGTGAACCCCGTCTCTACTAAAAATACAAAAATTAGCTGGGCATGTTGGCAGG
CGCCTGTAATCTACTACTTTGGGAAGCTGAGGCAGGAGAATCACTTGAACCTGGGAGACGG
AGGTTGCAGTGAGCCAAGATCACACCATTGCACGCCAGCCTGGGCAACAAAGCGAGACTCCA
TCTCAAAAAAAATCTCTCAAAATGGGTTGGGTGTCTGTAATCCAGCAGTCTTGGGAGGCTA
AGGTGGGTGGATTGCTTTGAGCCAGGAGTTGAGACACAGCTGAGGCAACATGGTGAACCC
ATCTCTACAAAAAATACAAACATAGCTGGGCTTGGTGGTGTGTGCTGTAGTCCAGCTGT
CAGACATTTAAACAGAGCAACTCCATCTGGAATAGGAGCTGAATAAAATGAGGCTGAGACC
TACTGGGCTGCATTCTCAGACAGTGGAGGCATTCTAAGTCACAGGATGAGACAGGAGGTCCG
TACAAGATACAGGTACATAAAGACTTTGCTGTATAAAACAGATTGCAGTAAAGAAGCCAACCAA
ATCCCACCAAAACCAAGTTGGCCACGAGAGTCACTCTGGTGTCTCTACTGCTACACTCTCT
GACAGCACCATGACAGTTTACAAATGCCATGGCAACATCAGGAAGTATCCCGATATGTCCCA
AAAGGGGGAGGAATGAATAATCACCCCTTGTTTAGCAAAATAGCAAGAATAACCATAAAA
GTGGGCAACAGCAGCTCTAGGCGCTGCTCTGTCTAGGAGTAGCCATTCTTTTGTCTCTT
TACTTTCTTAATAAACCTTGCTTTACCTTAAAAAAA

FIGURE 93

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA54002

><subunit 1 of 1, 544 aa, 1 stop

><MW: 60268, pI: 9.53, NX(S/T): 3

MLLPLLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYWFK
AVTETTTKGAPVATNHQSREVESTRGRFQLTGDPKAGNCSLVIRDAQMDESQYFFRVERGS
YVTYNFMNDGFFLKVTLSFTPRPQDHNTDLTCHVDFSRKGVSAQRTVRLRVAYAPRDLVIS
ISRDNTPALEPQPQGNVPYLEAQKGQFLRLCAADSQPPATLSWVLQNRVLSSSHHPWGRPL
GLELPGVKAGDSGRYTCRAENRLGSQQRALDLSVQYPPENLRVMVSQANRTVLENLGNGTSL
PVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHEGEFTCHARHP
LGSQHVSLSLSVHYKKGLISTAFSNGAFLGIGITALLLFLCLALIIMKILPKRRTQTETPRPR
FSRHSTILDYINVVPTAGPLAQKRNQKATPNSPRTPPPPGAPSPESKKNQKKQYQLPSFPEP
KSSTQAPESQESQEELHYATLNFPGVVRPRPEARMPKGTQADYAEVKFQ

Important features:

Signal peptide:

amino acids 1-15

Transmembrane domain:

amino acids 399-418

N-glycosylation site.

amino acids 100-103, 297-300 and 306-309

Immunoglobulins and major histocompatibility complex proteins signature.

amino acids 365-371

FIGURE 95

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53906

><subunit 1 of 1, 772 aa, 1 stop

><MW: 87002, pI: 4.64, NX(S/T): 8

MNCYLLLRFMLGIPLLWPCLGATENSQTKKVKQPVRSHLRVKRGWVWNQFFVPEEMNTTSHH
IGQLRSDLNNGNNSFQYKLLGAGAGSTFIIDERTGDIYAIQKLDREERSLYILRAQVIDIAT
GRAVEPESEFVIKVS DINDNEPKFLDEPYEAIVPEMSPEGLTVIQVTASDADDPSSGNNARL
LYSLLQGQPYFSVEPTTG VIRISSKMDRELQDEYVWIIQAKDMIGQPGALSGTTSVLIKLSD
VNDNKPIFKESLYRLTVSESAPTGTSGITIMAYDNDIGENAEMDYSIEEDDSQTFDIITNHE
TQEGIVILKKKVDFEHQNHYGIRAKVKNHHVPEQLMKYHTEASTTFIKIQVEDVDEPPLFL
PYYVFEVFEETPQGSFVGVSATDPDNRKSPIRYSITRSKVFNINDNGTITTSNSLDREISA
WYNLSITATEKYNIEQISSIPLYVQVLNINDHAPEFSQYYETYVCENAGSGQVIQTISAVDR
DESIEHHFYPNLSVEDTNNSSFTIIDNQDNTAVILTNRTGFNLQEEPVFYISILIADNGIP
SLTSTNTLTIHVDCDGSSTQTCQYQELVLSMGFKTEVIIAILICIMIIFGFIFLTGLKQ
RRKQILFPEKSEDFRENI FQYDDEGGGEEDTEAFDIAELRSSTIMRERKTRKTTSAEIRSLY
RQSLQVGPDSAIFRKFILEKLEEANTDPCAPPFDSLQTYAFEGTGLAGLSLSSLESASVSDQD
ESYDYLNELGPRFKRLACMFGSAVQSNN

Important features:

Signal peptide:

amino acids 1-21

Transmembrane domain:

amino acids 597-617

N-glycosylation sites.

amino acids 57-60, 74-77, 419-423, 437-440, 508-511, 515-518,
516-519 and 534-537

Cadherins extracellular repeated domain signature.

amino acids 136-146 and 244-254

[illegible][illegible]

FIGURE 97

GCAACCTCAGCTTCTAGTATCCAGACTCCAGCGCCGCCCGGGCGCGGACCCCAACCCGAC
 CCAGAGCTTCTCCAGCGGGCGCGCAGCGAGCAGGGCTCCCCGCTTAACTTCTCCGCGGGG
 CCCAGCCACCTTCCGGGAGTCCGGGTTGCCCACTCTCGCCTTCTGCACCTGCCA
 CCCCTGAGCGAGCGGGGCCCGAGCGAGTCA**ATGGCC**AACGCGGGGCTGCAGCTGTTGGGC
 TTCATTCTCGCCTTCTGGGATGGATCGGCGCCATCGTCAGCACTGCCTTGCCCCAGTGGAG
 GATTTACTCCTATGCGGGCGACAACATCGTGACCGCCAGGCCATGTACGAGGGGCTGTGGA
 TGTCTGCGTGTGCGAGAGCACCGGGCAGATCCAGTGCAAAAGTCTTTGACTCCTTGTGTAAT
 CTGAGCAGCACATTTGAAGCAACCCGTGCCCTTGATGGTGGTTGGCATCCTCCTGGGAGTGAT
 AGCAATCTTTGTGGCCACGTTGGCATGAAGTGATGAAGTGCTTGAAGACGATGAGGTGC
 AGAAGATGAGGATGGCTGTCAATTGGGGGTGCGATATTTCTTCTGCAGGTCTGGCTATTTTA
 GTTGCCACAGCATGGTATGGCAATAGAATCGTTCAGAAATTTCTATGACCCCTATGACCCAGT
 CAATGCCAGGTACGAATTTGGTCAGGCTCTCTTCACTGGCTGGGCTGTGCTTCTCTCTGCC
 TTCTGGGAGGTGCCCTACTTTGTGTTCTCTGTCCCCGAAAAACAACCTCTTACCCAACACCA
 AGGCCTATCCAAAACCTGCACCTTCCAGCGGGAAAGACTACGT**GTG**ACACAGAGGCAAAAG
 GAGAAAAATCATGTTGAAACAAACCGAAATGGACATTGAGATACATTATTAACATTAGGAC
 CTTAGAAATTTGGGTATTGTAATCTGAAGTATGGTATTACAAAACAAACAAACAAACAAAA
 ACCCATGTGTTAAAATACTCAGTGCTAAACATGGCTTAATCTTATTTTATCTTCTTTCTCA
 ATATAGGAGGGAAGATTTTTCATTTGTATTACTGCTTCCCATGGTCAAGTAATCATACTCAAAAT
 GGGGGAAGGGGTGCTCCTTAAATATATATAGATATGTATATACATGCTTTTTCTATATAAA
 ATAGACAGTAAAAATACTATTTCTCATTATGTTGATACAGCATACTTAAATATCTTCAAAAT
 AGGTAATGTATTTAATTCATATTTGATGAAGATGTTTATTGGTATATTTTCTTTTTCGTCC
 TTATATACATATGTAAACAGTCAAAATATCATTTACTCTTCTTATTAGCTTTGGGTGCCCTTG
 CCACAAGACCTAGCCTAAATTTACCAAGGATGAATTTTCAATTCCTTATGCGTGCCCTTTT
 CATATACTTATTTTATTTTACCATAATCTTATAGCACTTGCACTGTTATTAAGCCCTTAT
 TTGTTTTGTGTTTTCATTGGTCTCTATCTCCTGAATCTAACACATTTATAGCCTACATTTTA
 GTTTCTAAAGCCAAGAAGAAATTTATTACAAATCAGAACTTTGGAGGCCAAATCTTCTGCATG
 ACCAAAGTGATAAATTCCTGTTGACCTTCCACACAATCCCTGTACTCTGACCCATAGCACT
 CTTGTTTGTCTTTGAAAATATTTGTCCAATTGAGTAGCTGCATGCTGTTTCCCCAGGTGTTGT
 AACACAACCTTTATTGATTGAATTTTAAAGCTACTTATTATAGTTTTATATCCCCCTAAACT
 ACCTTTTTGTTCGCCATTCCCTTAATTGTATTGTTTTCCCAAGTGTAATTATCATGCGTTTTTA
 TATCTTCTAATAAGGTGTGGTCTGTTTGTCTGAACAAAGTGCTAGACTTTCTGGAGTGATA
 ATCTGGTGACAAAATTTCTCTCTGTAGCTGTAAAGCAAGTCACTTAATCTTTCTACCTCTTTT
 TTCTATCTGCCAAATTTGAGATAATGATACTTAACCAAGTTAGAAGAGGTAGTGTGAATATTAA
 TTAGTTTATATTACTCTTATTTCTTTGAACATGAACATGCGCTATGTAGTGTCTTATTGTGCT
 CAGCTGGCTGAGACACTGAAGAAGTCACTGAACAAACCTACACAGTACCTTCATGTGATT
 CACTGCTTCCCTCTCTACCAAGTCTATTTCCTAGCAACAAACCTACACACATACCTTCAT
 GTGGTTCACTGCTTCCCTCTCTTACCAGTCTATTTCCTAGAACAAACCTACGCACATAC
 CTTATGTGGCTCAGTGCTTCTCTCTCTACCACTTATTTCCTATCTTTCAGCTGTGTCT
 GACATGTTTGTGCTCTGTTCCATTTTAAACAACCTGCTCTTATTTCCTAGTCTGTACAGAATG
 CTATTTCACTTGAGCAAGATGATGTAATTGAAAGGGTGTGGCACTGGTGTCTGGAGACCTG
 TATTGAGCTTGGTGTCTATCAATCACCGCTCTGTGTTTGGAGCAAGGCATTGGCTGCTGTAA
 GCTTATTGCTTCATCTGAAGCGGTGGTTTGAATTCCTGATCTTCCCACTCACAGTCAATG
 TTGTTGGGATCCAGTGAGATAGAATACATGTAAGTGTGGTTTTGTAATTTAAAAAGTGCTAT
 ACTAAGGGAAGAATTTGAGGAATTAACTCGATACGTTTTGGTGTGCTTTTCAATGTTTGA
 AAATAAAAAAATGTTAAG

1037036-102401

FIGURE 98

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52185

><subunit 1 of 1, 211 aa, 1 stop

><MW: 22744, pI: 8.51, NX(S/T): 1

MANAGLQLLGFI¹LAFLGWIGAI²VSTALPQWRIYSYAGDNIVTAQ³AMYEGLWMSCV⁴SQSTGQI⁵
QCKVFD⁶SLNLSSTLQATRALMVVGILLGVIAIFVATVGMKCMKLE⁷DEVQKMRMAVIGGA⁸
IFLLAGLAILVATAWYGNRIVQ⁹EFYDPMTFPVNARYEFGQALFTGWAAASLCLLGGALLCCSC¹⁰
PRKTT¹¹SYPTPRPYPKPAPSSGKD¹²YV

Important features:

Signal peptide:

amino acids 1-21

Transmembrane domains:

amino acids 82-102, 118-142 and 161-187

N-glycosylation site.

amino acids 72-75

PMP-22 / EMP / MP20 family proteins

amino acids 70-111

ABC-2 type transport system integral membrane protein

amino acids 119-133

FIGURE 99

TTCTGGCCAAACCCGGGGCTNCAGCTGTTGGGCTTCATCTCGCCTTCTCTGGGATGGATCGGC
GCCATCNTCACACTGCCCTTCCCCAGTGGAGGATTTTACTCCCTATGCTGGCGACAACATCG
TGACCGCCCAGCCCATGTACGAGGGGCTGTGGATGTCCNGCGTGTGCGAGAGCACCGGGCAG
ATCCAGTGCAAAGTCTTTGACTCCTTGCTGAATCTGAGCAGCACATTGCAAGCAACCCGTGC
CTTGATGGTGGTTGGCATCCTCCTGGGAGTGATAGCAATCTTTGTGGCCACCGTTGGCATGA
AGTGTATGAAGTGCTTGAAGACGATGAGGTGCAGAAGATGAGGATGGCTGTCATTGGGGGC
GCGATATTTCTTCTTGCCAGGTCTGGCTATTTTAGTTGCCACAGCATGGTATGGCAATAGAA
CNTTCAACANTTCTATGACCCTATGACCCAGTCAATGCCAGGTACGAATTTGGTCA
GGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTCTGCCTTCTGGGAGGTGCCCTACTTTGCT
GTTCTGTCCC

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FIGURE 100

ACCCTTGACCCAACGCGGCCCGGACCGNTTCATGGCCAAACGCGGGNCTCCAGCTGTTGG
GCTTCATTCTCCCCTTCTGGGATGGACCGGCGCCCATNTCAGCACTGCCCTGCCCCAGTG
GAGGATTTACTCCTATNCCGGCNACAACATCGTGACCGCCCAGGCCNTGTACGAGGGGCTGT
GGATGTCCTGCGTGTGCGAGAGCACCGGGCAGATCCAGTGCAAAGTCTTTGACTCCCTTGCT
GAATCTGAGCAGCACATTGCAAGCAACCCGTGCCITGATGGTGGTTGGCATCCTCCTGGGAG
TGATAGCAATCTNNNTGGCCACCGTTGTNNNTGAAGTGTATGAAGTGCTTGGAAGACGATGA
GGTGCGAGAAGATGAGGATGGCTGTCATTGGGGGCGCGATATTCTTCTTGCAAGGTCTGGCTA
TTTTAGTTGCCACAGCATGGTATGGCAATAGAATCGTTCAAGAATTCTATGACCCTATGACCGA

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FIGURE 101

GGGCCCCGACCATTATCCAACCGGGNTCACTGTTGGCTCATCTCCCTCCTGGATGAANCGCGC
CATCNTCAGACTCCCTGCCCCATGGAGATTNNCCTATGCTGGCGACAACATCNTGACCCCC
AGCCATGTACGAGGGGCTTTGAACGTCNGCGTGTGCGAGANACCGGGCAGATCCAGTGCAA
AGTCTTTGACTCCTTGCTGAATCTGNGCAGCACATTGCAGCAACCNTGCCCTGATGGTGGT
TGGCATCCTCCTGGGAGTGATAGCAATCTTTGTGGCCACCGTTGGCATGAAGTGTATGAAGT
GCTTGAAGACGATGAGGTGCAGAAGATGAGGATGGCTGTCAATTGGGGGCGCGATATTCTT
CTTGCAAGGTCTGGCTATTTNNNGTTGCCACAGCATGGTATGGCAATAGAATCGTTCAAGAAT
TCTATGACCCCTATGACCCAGTCAATGCCAGGTACGAATTTGGTCAGGCTCTCTTCACTGGC
TGGGCTGCTGCTTCTCTCTGCCTTCTGGGAGGTGCCCTACTTTGCTGTTCTTGCGA

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FIGURE 102

ATTCTCCCCCTCTGGATGGATCGCNCCACCGTCACATTGCCTTCCCCCANTGGAGGATTNAC
TCCTATGCTGGCGACAACATCGTGACCCCCCAGGCCATTTACCGAGGGGCTTTGGATGTCNT
GCNTGTGCGAGAGCACCGGGCAGATCCCAGTGCAAAGTCTTTGACTCCTTGCTGAATCTGAG
CAGCACATTGCAAGCAACCCGTGCCTTGATGGGGTTGGCATCCTCCTGGGAGTGATAGCAAC
CTTTGTGGCCACCGTTGGCATGAAGTGATGAAGTGCTTGAAGACGATGAGGTGCCAGAAG
ATGAGGATGGCTGTCATTGGGGGCGCATATTTCTTGTTCAGGCTCTGGCTATTTTAGTNGC
CACAGCATGGTATGGCAATAGANTNNNTTCNNGNNNTCTATGACCCATGACCCAGTCAATG
CCAGGTACGAATTTGGTCAGGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTCTGCCTTCTG
GGAGGTGCCCTACTTTGCTGTTCCCTGTCCC

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FIGURE 103

AGAGCACCGGCAGATCCCAAGTCTTTGACCCCTTGCTGAATCTGAGCAGCACATTNC
AAGCAACCCCTTGCCCTTGAGGTGGTTGNCATCCCCCTGGGAGTGAATAGCAATCTTTGTG
GCCACCGTTGGCATGAAGTNTATGAAGTGTCTGGAAGACGATGAGGTGCAGAAATGAGGAT
GGCTGTCAATGGGGGCGCGATATTTCTTCTTGACGGTCTGGCTATTTTAGTNNCCACAGCAT
GGATATGGCAATAGNATNNNTTCGNGGNTTCTATGACCCATATGACCCAGTCAATGCCAGGTAC
GAATTTGGTCAGGCTCTCTTACGCTGGGCTGCTGCTTCTCTGCTCTTGGGAGGTGC
CCTACTTTGCTGTTCTCTGCTCCCGAA

[illegible]

Age	Sex	Height (cm)	Weight (kg)	Body mass index (kg/m ²)	Waist circumference (cm)	Waist-hip ratio	Waist-hip ratio (cm)
18	M	175	75	24.2	95	0.85	78
20	F	165	55	20.1	85	0.85	72
22	M	180	85	26.3	100	0.85	85
24	F	170	65	22.6	90	0.85	78
26	M	185	95	27.8	105	0.85	90
28	F	175	75	24.2	95	0.85	78
30	M	190	105	29.7	110	0.85	95
32	F	180	85	26.3	100	0.85	85
34	M	195	115	30.8	115	0.85	100
36	F	185	95	27.8	105	0.85	90
38	M	200	125	31.2	120	0.85	105
40	F	190	105	29.7	110	0.85	95
42	M	205	135	32.3	125	0.85	110
44	F	195	115	30.8	115	0.85	100
46	M	210	145	33.3	130	0.85	115
48	F	200	125	31.2	120	0.85	105
50	M	215	155	34.4	135	0.85	120
52	F	205	135	32.3	125	0.85	110
54	M	220	165	35.4	140	0.85	125
56	F	210	145	33.3	130	0.85	115
58	M	225	175	36.4	145	0.85	130
60	F	215	155	34.4	135	0.85	120
62	M	230	185	37.4	150	0.85	135
64	F	220	165	35.4	140	0.85	125
66	M	235	195	38.4	155	0.85	140
68	F	225	175	36.4	145	0.85	130
70	M	240	205	39.4	160	0.85	145
72	F	230	185	37.4	150	0.85	135
74	M	245	215	40.4	165	0.85	150
76	F	235	195	38.4	155	0.85	140
78	M	250	225	41.4	170	0.85	155
80	F	240	205	39.4	160	0.85	145
82	M	255	235	42.4	175	0.85	160
84	F	245	215	40.4	165	0.85	150
86	M	260	245	43.4	180	0.85	165
88	F	250	225	41.4	170	0.85	155
90	M	265	255	44.4	185	0.85	170
92	F	255	235	42.4	175	0.85	160
94	M	270	265	45.4	190	0.85	175
96	F	260	245	43.4	180	0.85	165
98	M	275	275	46.4	195	0.85	180
100	F	265	255	44.4	185	0.85	170

AGCAATGCCCTGCCCCAGTGGAGGATTAATTCCTATGNTGGGGACAACATTGTGACNCGCC
AGGCCATGTACGGGGGCTGTGGATGTCTGCGTGTGCGAGACACCGGCAGATCCAGTGC
AAAGTNTTTGACTCCTTGCTGAATTTGAGCAGACATTGCAAGCAACCCGTGCCTTGATGGT
GGTTGGCATCTTCCTGGGAGTGATAGCAATCTTTGTGGCCACCGTGGNAATGAAGTGTATGA
AGTGCTTGAAGACGATGAGGTGCAGAAGATGAGGATGGCTGTGATTGGGGCGCGATATTT
CTNTTTCAGGTTCTGGCTATTTTAGTTGCCACAGCATGGAATGTGGCAATGAATNNTTCAAGA
ATTTTATGACCCATACCCCTCAATGCCAGGTACGAATTTGGTCAGGCTTTNTTCACTG
GCTGGGCTGCTGCTTNTTCTGCTTNTGGGAGGTGCCCTANTTTGCTGTTCTGCGCAAC

FIGURE 105

TCATAGGGGGCGCGATATTTTCTTGCAGGINTGGTTATTTTAGTTGCCACAGCATGGTA
TGGCAATAGAAATCGTTCAAGAATTNTATGACCCCTATGACCCAGTCAATGCCAGGTACGAAT
TTGGTCAGGCTCTNTTCACTGGNTGGGCTGCTGCTTCTNTNNGCCTTNTGGGAGGTGCCCTA
CTTGCTGTTCTG

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FIGURE 106

TTCTCTGGGATGGATCCGCCCCATCNTCACATGCCCTGCCCNTGGAGATTTACNCCTATGC
TGGCGAACAAACATCNTGACCGCCCAGGCCATGTACGAGGGGCTGTGGAATGTCCTGCGTGTG
CCAGAGCACCGGGCAGATCCAGTGC AAAGTCTTTGACTCCTTGCTGAATCTGAGCAGCACAT
TGCAAGCAACCN TGCCCTTGATGGTGGTTGGCATCCTCCTGGGAGTGATAGCAATCTTTGTGG
CCACCGTTGGCATGAAAGTGTATGAAGTGCTTGAAGACGATGAGGTGCAGAAGATGAGGAT
GGCTGTCAATTGGGGGCGCGATATTTCTTCTTGCAAGTCTGGCTATTTTAGNNGCCACAGCAT
GGTATGGCAATCAGACCCNNTCANAAACTCTATGACCCCTATGACCCAGTCAATGCCAGGTA
CGAATTGGTCAGGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTGCTTCTGGGAGGTG
CCCTACTTTGCTGTTCTCTGTCCCCGAAAAACAACCTCTTACCCACG

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CGGGGCTGCAGCTGTGTGGGCTTCATCTCGCTTCTCTGGGATGGAAATCGGCGCCATCGTCAGCA
CTGCCCTGCCCATGAGGATTACTCNTATGCTGGCGACAACATCGTGACCNCCAGGCCA
TGTAACAGGGGGCTGTGGATGTCNGCGTGTGCGAGAGCACCGGGCAGATCCAGTGCAAAGTCT
TTGACTCCTTGCTGAATCTGAGCAGCACATTGCAAGCAACCTGCGCTTGATGGTGGTTGGCA
TCCTCCTGGGAGTGATAGCAATCTTTGTGGCCACCGTTGGCATGAAGTGATGAAGTGCTTG
GAAGACGATGAGGTGCAGAAGATGAGGATGGCTGTCAATGGGGGCGCGATATTTCTTCTTGC
AGGCTCTGGCTATTTNTAGTTGCCACGACATGGTATGGCACAATAAGATCTGTTCAAGAATTCTAT
GACCCATAGTACCCCACTCAATGSCAGGTACGAATTTGGTCAGGCTCTTCTTCACTGGCTGGGC
TGCTGCTTCTCTCTGCTTCTCTGGGAGGTGCCCTACTTTGCTGTTTCTCTGCGAA

FIGURE 108

GCGTGCCGTCAGCTCGCGGGGACCGCGGCTCGCCCTCGCCCTCCGCCCTGCGCCTGCAC
CGCGTAGACCGACCCCCCTCCAGCGCGCCACCCGGTAGAGGACCCCCGCGCGCCCG
ACCGGTCCCCGCGCTTTTGTAAAACTTAAAGCGGGCGCAGCATTACCGTTCCCGCCCCGGT
GACCTCTCAGGGGTCTCCCCGCCAAAGGTGCTCCGCGCTAAGGAACATGGCGAAGGTGGAG
CAGGTCTGAGCCTCGAGCCCGAGCAGCAGCTCAAATCCGAGGTCCCTTCACCGATGTTGT
CACCACCAACCTAAAGCTTGGCAACCCGACAGACCGAAATGTGTGTTTAAAGTGAAAGACTA
CAGCACCCAGTAGGTACTGTGTGAGGCCCAACAGCGGAATCATCGATGCAAGGGCCCTCAATT
AATGTATCTGTGATGTTACAGCCCTTCGATTATGATCCCAATGAGAAAAAGTAAACACAAGTT
TATGTTTCAGTCTATGTTTGCTCCAACCTGACACTTCAGATATGGAAGCAGTATGGAAGGAGG
CAAAACCGGAAGACCTTATGGATTCAAAACTTAGATGTGTGTTTGAATTGCCAGCAGAGAAT
GATAAACCATGATGATGATAAATAAATAAATATATCCCAACTGCATCAAAGACAGAAAC
ACCAATAGTGCTCTAAGTCTCTGAGTTCTTCTTGATGACACCGAAGTTAAGAAGGTTATGG
AAGAATGTAAGAGGCTGCAAGGTGAAGTTCAGAGGCTACGGGAGGAGAAACAAGCAGTTCAG
GAAGAAGATGGACTGCGGATGAGGAAGACAGTGCAGAGCAACAGCCCCATTTACGATTAGC
CCCAACTGGGAAGGAAGAAGGCCTTAGCACCCGGCTCTTGGCTCTGGTGGTTTGTCTTTA
TCGTTGGTGTAATTATTTGGGAAGATTGCCTTGTAAGGTAGCATGCACAGGATGGTAAATTG
GATTGGTGGATCCACCATATCATGGGATTTAAATTTATCATAACCATGTGTAAAAAGAAATT
AATGTATGATGACATCTCACAGGTCTTGCCCTTTAAATTACCCCTCCCTGCACACACATACAC
AGATACACACACAAATATAATGTAACGATCTTTTAGAAAGTTAAAAATGTATAGTAACTG
ATTGAGGGGGAAAAAGAATGATCTTTATTAATGACAAGGAAACCATGAGTAATGCCAAT
GGCATATTGTAATGTCAATTTTAAACATTGGTAGGCCCTTGGTACATGATGCTGGATTACCTC
TCTTAAAAAGACCCCTTCTCGCCTGTTGGTGCTGGCCCTTGGGGAGCTGGAGCCAGCAT
GCTGGGGAGTGCGGTGAGCTCCACACAGTAGTCCCCACGTGGGCCACTCCCGGCCAGGCTG
CTTTCCGTGCTCTTCAGTTCTGTCCAAGCCATCAGCTCCTTGGGACTGATGAACAGAGTCAGA
AGCCCAAGGAATTGCACTGTGGCAGCATCAGACGTACTCGTCATAAGTGAGAGGCGGTGTGT
TGACTGATTGACCCAGCGCTTTGGAAATAAATGGCAGTGCTTTGTTCACTTAAAGGACCA
GCTAAATTTGATTTGGTTCATGTAGTGAAGTCAAACCTGTATTAGAGATGTTTAAATGCATA
TTTAACCTTATTTAATGTATTTTCACTCATGTTTCTTATTGTGCAAGAGTACAGTTAATGC
TGCGTGCTGCTGAACTCTGTTGGGTGAACTGGTATTGCTGCTGGAGGGCTGTGGGCTCCTCT
GTCTCTGGAGAGTCTGGTCATGTGGAGGTGGGGTTTATTGGGATGCTGGAGGAAGAGCTGCCA
GGAAGTGTTTTCTGGGTGAGTAAATAACAACCTGTCATAGGGAGGGAAATTTCTCAGTAGTG
ACAGTCAACTCTAGGTTACCTTTTTTAAATGAAGAGTAGTCAGTCTTCTAGATTGTTCTTATA
CCACCTCTCAACCATTAATCACTTCCAGCGCCAGGTCCAAGTCTGAGCCTGACCTCCCC
TTGGGGACCTAGCCTGGAGTCAGGACAAATGGATCGGGCTGCAGAGGGTTAGAAGCGAGGGC
ACCAGCAGTTGTGGGTGGGGAGCAAGGGAAGAGAGAACTCTTCAGCGAATCCTTCTAGTAC
TAGTTGAGAGTTTGACTGTGAATTAATTTATGCCATAAAGACCAACCCAGTCTGTTTGA
CTATGTAGCATCTTGAAGAAGAAAATTATAATAAGCCCCAAAATTAGAAAA

FIGURE 109

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53977

<subunit 1 of 1, 243 aa, 1 stop

<MW: 27228, pI: 7.43, NX(S/T): 2

MAKVEQVLSLEPQHELKFRGPFSTDVVTNLKLGNPTRNVCFKVKTTAPRRYCVRPNSGIID
AGASINVSVMQLQPFDDPNEKSKHKFMVQSMFAPTDTSMEAVWKEAKPEDLMSKLRGVFE
LPAENDKPHDVEINKIISTTASKTETPIVSKSLSSSLDDTEVKKVMEECKRLQGEVQRLREE
NKQFKEEDGLRMRKTVQSNPISALAPTGKEEGLSTRLLALVVLFFIVGVIIGKIAL

Important features:

Transmembrane domain:

amino acids 224-239

N-glycosylation site.

amino acids 68-71

N-myristoylation site.

amino acids 59-64, 64-69 and 235-240

FIGURE 110

GTCAGTCTTCTAGATTGTCCTTATCCCACCTTTCAACCANTACTCACATTTTCNAGCGCCCAG
GTCCANGTCTGAGCCTGACTTCCCCTTGGGGACCTAGCCTGGAGTCAGGACAATGGNTCGGG
CTGCAGAGGNTTAGAAGCGAGGGCACCAGCAGTTTGGGTGGGGAGCAAGGGNNGAGAGAAA
CTCTTCAGCGAATCCTTCTAGTACTAGTTGAGAGTTTGACTGTGAATTAATTTTATGCCATA
AAAGACNAACCCAGTTCTGTTTGACTATGTAGCATCTTGAAAAGAAAAATTAATAAAGCC
CCTAAAATTAAGAATTCTTTTGTCAATTTGTGCATTTGCTCTATGGGGGAATTATTATTTT
ATCATTTTTATTATTTTGCCATTGGAAGGTTAACTTTAAAATGAGC

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FIGURE 111

TATTGTAAAGGCCATTTTAAACCATTGGTAGGCCTTGGTACATGATGCTGGATTACCTCCTT
AAATGACACCNNTTCCTCGCCTGTTGGTGCTGGCCNNTGGGGAGCTGGAGCCCAGCATGCTG
GGGAGTGCGGTCAGCTCCACACAGTAGTCCCCACGTGGCCCACTCCCGGCCCAGGCTGCTTT
CCGTGTCTTCAGTTCCTGTCCAAGCCATCAGCTCCTTGGGACTGATGAACAGAGTCAGAAGCC
CAAAGGAATTGCCACTGTGGCAGCATCAGACGTACTCGTCATAAGTGAGAGGCGTGTGTTGA
CTGATTGACCCAGCGCTTTGGAAATAAATGGCAGTGCTTTGTTCACTTAAAGGGACCAAGCT
AAATTGTATTGGTTCATGTAGTGAAGTCAAAGTCTTATTTCAGAGATGTTTAAATGCATATTTA
ACTTATTTAATGTATTTTCATCTCATGTTTTCTTATTGTCACAAGAGTACAGTTAATGCTGCG
TGCTGCTGAACCTCTGTTGGGTGAACCTGGTATTGCTGCTGGAGGGCTG

[illegible]

TGCTTTCCGTGTCCTTCAGTTCTGTCCAAGCCATCAGCTCCTTGGGACTTGATGAACAGAGTC
 AGAAGCCCAAAGGAATTGCACGTGTGGCAGCATCAGACGTA CTCTGCATCAAGTGAGAGGCGTG
 TGTTGACTGATTGACCAGCCTTTGGAATAAATGGCAGTGCTTTTGTTCACTTAAAGGGAC
 CAAGCTAAATTTGTATTGGTTTCATGTAGTGAAGTCAAACGTTATTACAGAGATGTTTAATGC
 ATATTTAACTATTATTAATGTATTTCACTCATGTTTTCTATTGTGCACAAGAGTACAGTTAA
 TGCTGCGTGC

FIGURE 115

AAACCTTTAAAAGTTGAGGGGAAAAGAATGATCCTTTATTAAATGACAAGGGAAACCN TGNGT
AATGCCACAATGGCATATTGTAAATGTCATTTTAAACATTTGGTAGGCCTTGGTACATGATGC
TGGATTACCTCTCTTTAAAATGACACCCCTTCCTCGCCTGTTGGTGCTGGCCCTTGGGGAGCTN
GAGCCCAGCATGCTGGGGAGTGCGGTCTGCTCCACACAGTAGTCCCCANGTGGCCCANTCCC
GGCCCAGGCTGCTTTCCTGTCTTCAGTTCTGTCCAAGCCATCAGCTCCTTGGGANTGATGA
ACAGAGTCAGAAGCCCAAAGGAATTGCANTGTGGCAGCATCAGANGTANTNGTCATAAGTGA
GAGGCGTGTGTTGANTGATTGACCCAGCGCTTTGGAAATAAATGGCAGTGCTTTGTTCANTT
AAAGGNC CAAGNTAAATTTGTATTGGTTCATGTAGTGAAGTCAAANTGTTATTTCAGAGATG
TTTAATGCATATTTAANTTATTTAATGTATTTTCATNTCATGTTTTCTTATTGTCACAAGGGT
ACAGTTAATGCTGCGTGCTGCTGAANTCTGTTGGGTGAANTGGTATTGCTG

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FIGURE 116

GGCCCTTGGGGAGCTGGAGCCCAGCATGCTGGGGAGTGCGGTCAGCTCCACACAGTAGTCCC
CACGTGGCCCACTCCCGGCCAGGCTGCTTCCGTGTCTTCAGTTCTGTCCAGCCATCAGC
TCCTTGGGACTGATGAACAGAGTCAGAAGCCCAAAGGAATTGCACCTGTGGCAGCATCAGACG
TACTCGTCATAAGTGAGAGGCGTGTGTTGACTGATTGACCCAGCGCTTTGGAATAAATGGC
AGTGCTTTGTTCACTTAAAGGGACCAAGCTAAATTTGTATTGGTTCATGTAGTGAAGTCAAA
CTGTTATTTCAGAGATGTTTAATGCATATTTAACTTATTTAATGTATTTTCATCTCATGTTTT
TTATTGTCACAAGAGTACAGTTAATGCTGCGTGCTGCTGAACTCTGTTGGGTGAACTGGTAT
TGCTGCTGGAGGGCTGTGGGCTCCTCTGTCTCTGGAGAGTCTGGTCATGTGGAGGTGGG

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FIGURE 117

GCAGAGCTCCGGGTGCTGTGGCCCGGCCTTGGCGGGCGGCCCTCCGGCTCAGGCTGGCTGAGA
GGCTCCCAGCTGCAGCGTCCCCGCCCGCCTCCTCGGGAGCTCTGATCTCAGCTGACAGTGCC
CTCGGGGACCAAAACAAGCCTGGCAGGGTCTCACTTTGTGGCCAGGCTGGAGTTCACTGAGCA
TGATCATGGTTTACTGCAGCCTTGACCTCCTGGGTTCAAGCATCTCTGTAGTAGCTGGGA
CTACAGGACAAAATTAGAAGATCAAAATGGAAAAATATGCTGCTTTGGTTGATATTTTTACC
CCTGGGTGGACCTCATTGATGGATCTGAAATGGAATGGGATTTTATGTGGCACTTGAGAAA
GGTACCCCGGATTGTCAAGTAAAGGACTTTCCATCTCACCAGCCCCGATTGTAGGCGAGTG
CTAAGATGATGGTAAATACAGTGTGTGGCATCGAATGCCAGAAAGAACTCCCAACTCCAGC
CTTTCTGAATTGGAGATTATCTTTCCCTATGAGACTGTCTTTGAGAATGGCACCCGAACTTT
AACCAGGGTGAAAGTTCAAGATTTGGTTCTTGAGCCGACTCAAAATATCACCAAAAGGGAG
TATCTGTTAGGAGAAAAGACAGGTGTATGGCACCGACAGCAGGTTCAAGCATCTTGACAAA
AGGTTCTTAACCAATTTCCCTTTCAAGCACAGCTGTGAAGCTTTCCACGGGCTGTAGTGCCAT
TCTCATTTCCCTCAGCATGTTCTAACTGCTGCCACTGTGTTTATGATGGAAGGACTATG
TCAAAGGGAGTAAAAAGCTAAGGGTAGGGTTGTTGAAGATGAGGAATAAAAGTTGGAGGCAAG
AAACGTGAGGTTCTAAGAGGAGCAGGAGAGAAGCTAGTGGTGTGACCAAGAGAGGGTAC
CAGAGAGCATCTGCAGGAGAGAGCGAAGGGTGGGAGAAGAAAGAAAAAATCTGGCCGGGGTC
AGAGGATTGGCCGAAGGGAGGCTTCCCTTTCACTGGACCCGGGTCAAGAATACCCACATTCCG
AAGGGCTGGGCACGAGGAGGCATGGGGACGCTACCTTGGACTATGACTATGCTCTTCTGGA
GCTGAAGCGTGCTCAAAAAAGAAATACATGGAACCTTGAATCAGCCCAACGATCAAGAAAA
TGCTGGTGGAATGATCCACTTCTCAGGATTTGATAACGATAGGGCTGATCAGTTGGTCTAT
CGGTTTTCGATGTGTCCGACGAATCCAATGATCTCCTTTACCAATACTGCGATGCTGAGTC
GGCTCCACCGGTTGGGGGTCTATCTGCGTCTGAAAGATCCAGACAAAAGAAATTTGAAGC
GCAAAATCATTGCGGTCTACTCAGGGCACCAAGTGGGTGGATGTCACCGGGGTTCAGAAGGAC
TACAACGTTGCTGTTGCGATCACTCCCTAAAATACGCCAGATTGCGCTCTGGATTACGGG
GAACGATGCCAATTGTGCTTACCGCTTAACAGAGACCTGAAAAGGGCGGTTGATCATCTAAA
TCACAGAGAAAACCAAGCTCTGCTTACCCTAGTGAGATCACTTCATAGGTTATGCCCTGAGCTT
GAACCTCTGTCAATAGCATTTCACATTTTCAAATCAGGAGATTTTCGTCCATTTAAAAAA
TGATAGGTGCAGATATTGAAACTAGGTGGGCACTTCAATGCCAAGTATATACTCTTCTTTA
CATGGTGTAGGTTTCATTGTTAGAAAAATTTTGTGCGCTTCTTAAAAATTAGACACATTT
AAACCTTCAACAGGTATTATAAATAACATGTGACTCCTTAATGGACTTATTTCTCAGGGTCC
TACTCTAAGAAGAACTCAATAGGATGCTGGTTGTGTATTAAATGTGAAATTCATAGATAAA
GGTAGATGGTAAAGCAATTAGTATCAGAATAGAGACAGAAAGTTACAACACAGTTTGTACTA
CTCTGAGATGGATCCATTCAAGCTCATGCCCCAATGTTTATATTGTGTTATCTGTTGGGCTT
GGGACATTTAGTTTAGTTTTTTTGAAGAATTACAAATCAGAAGAAAAAGCAAGCATTTAA
CAAACTAATAACTGTTTTACTGCTTTAAGAAATAACAATTAATGTGTATTATTTAAAAA
TGGGAGAAATAGTTTTGTTCTATGAAATAAACCTAGTTTGAAGAAATAGGAAGCTGAGACATTT
TAAGATCTCAAGTTTTTATTAACTAATACTCAAAATATGGACTTTTCATGTATGCATAGGG
AAGACACTTCAAAATTTATGAATGATCATGTGTTGAAAGGCCAATTATTTATGCTATACAT
TCTATGTATGAGGTCTACATTTTATAGGACAAAGAAATCTGTAATCTTTTCAAGAAAGAGT
CTTTTCTCCTTGACAAAATCCAGCTTTTGTATGAGGACTATAGGGTGAATCTCTGATTAG
TAATTTTAGATATGTCCTTTCTTAAAAATGAATAAAATTTATGAATATGA

FIGURE 118

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57253

<subunit 1 of 1, 413 aa, 1 stop

<MW: 47070, pI: 9.92, NX(S/T): 3

MENMLLWLIFFTPGWTLIDGSEMEWDFMWHLRKVPRIVSERTFHLTSPAFEADAKMMVNTVC
GIECQKELPTPSLSELEDYLSYETVVFENGTRTLTRVKVQDLVLEPTQNITTGVSVRKRQV
YGTDSRFSILDKRFLTNFPFSTAVKLSTGCSGILISPQHVLTAACHCVHDGKDYVKGSKKLRV
GLLKMRNKSGGKKRRGSKRSRREASGGDQREGTREHLQERAKGGRRRKSGRGQRIAEGRPS
FQWTRVKNTHIPKGWARGGMDATLDYDYALLELKRAHKKKYMELGISPTIKKMPGGMIHFS
GFDNDRADQLVYRFCSVSDESNDLLYQYCDAESGSTGSGVYLRLKDPDKKNWKRKIIAVYSG
HQWVDVHGVQKDYNVAVRITPLKYAQICLWIHGNDANCAYG

Important features:

Signal peptide:

amino acids 1-16

N-glycosylation sites.

amino acids 90-93, 110-113 and 193-196

Glycosaminoglycan attachment site.

amino acids 236-239

Serine proteases, trypsin family, histidine active site.

amino acids 165-170

FIGURE 119

AATGTGAGAGGGGCTGATGGAAGCTGATAGGCAGGACTGGAGTGTTAGCACCCAGTACTGGAT
GTGACAGCAGGCAGAGGAGCACTTAGCAGCTTATTCAGTGTCCGATTCTGATTCGGCAAGG
ATCCAAGCATGGAATGCTGCCGTGCGGCAACTCCTGGCACACTGCTCCTCTTTCTGGCTTTT
CTGCTCCTGAGTTCCAGGACCGCACGCTCCGAGGAGGACCGGGACGGCCTATGGGATGCGT
GGGCCCATGGAGTGAATGCTCACGCACCTGCGGGGAGGGGCCTCCTACTCTCTGAGGCGCT
GCCTGAGCAGCAAGAGCTGTGAAGGAAGAAATATCCGATACAGAACATGCAGTAATGTGGAC
TGCCACCAGAAGCAGGTGATTTCCGAGCTCAGCAATGCTCAGCTCATAATGATGTCAAGCA
CCATGGCCAGTTTTATGAATGGCTTCTGTGTCTAATGACCCTGACAACCCATGTTCACTCA
AGTGCCAAAGCCAAAGGAACAACCTGGTTGTTGAACTAGCACCTAAGGTCTTAGATGGTACG
CGTTGCTATACAGAATCTTTGGATATGTGCATCAGTGGTTTATGCCAAATTGTTGGCTGCGA
TCACCAGCTGGGAAGCACCCTCAAGGAAGATAAAGTGTGGGTCTGCAACGGAGATGGGTCCA
CCTGCCGCTGGTCCGAGGGCAGTATAAATCCAGCTCTCCGCAACCAATCGGATGATACT
GTGGTTGCACTTCCCTATGGAAGTAGACATATTCGCCTTGTCTTAAAGGTCTGTATCACTT
ATATCTGGAACCAAAACCTCCAGGGGACTAAAGGTGAAAACAGTCTCAGCTCCACAGGAA
CTTTCTTGTGGACAATTCTAGTGTGGACTTCCAGAAATTTCCAGACAAAGAGATACTGAGA
ATGGCTGGACCACTCACAGCAGATTTCAATTGTCAAGATTCTGAATCGGGCTCCGCTGACAG
TACAGTCCAGTTCATCTTCTATCAACCATCATCCACCGATGGAGGGAGACGGATTTCTTTC
CTTGCTCAGCAACCTGTGGAGGAGGTTATCAGCTGACATCGGCTGAGTGCTACGATCTGAGG
AGCAACCGTGTGGTTGCTGACCAATACTGTCACTATTACCCAGAGAACATCAAACCCAAACC
CAAGCTTCAGGAGTGCAACTTGGATCCTTGTCAGCCAGTGACGGATACAAGCAGATCATGC
CTTATGACCTCTACCATCCCTTCCCTCGGTGGGAGGCCACCCATGGACCGGTGCTCCTCC
TCGTGTGGGGGGGCATCCAGAGCCGGGCAGTTTCTGTGTGGAGGAGGACATCCAGGGGCA
TGTCACCTTCAGTGAAGAGTGGAAATGCATGTACACCCCTAAGATGCCATCGCGCAGCCCT
GCAACATTTTTGACTGCCCTAAATGGCTGGCAAGGAGTGGTCTCCGTGCACAGTGACATGT
GGCCAGGGCCTCAGATACCGTGTGGTCTCTGCATCGACCATCGAGGAATGCACACAGGAGG
CTGTAGCCCAAAAACAAAGCCCCACATAAAAGAGGAATGCATCGTACCCATCCCTGCTATA
AACCCAAAGAGAAACTTCAGTCGAGGCCAAGTTGCCATGGTTCAAACAAGCTCAAGAGCTA
GAAGAAGGAGCTGCTGTGTGAGGAGGCCCTCGTAAGTGTGTAAGGACACAGACTGTTCTATA
TTTGAAACTGTTTTGTTTTAAAGAAAGCAGTGTCTCACTGGTTGTAGCTTTCATGGGTTCTGA
ACTAAGTGTAATCATCTCACCAAAGCTTTTTGGCTCTCAAATTAAAGATTGATTAGTTTCAA
AAAAAAAA

FIGURE 120

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58847
<subunit 1 of 1, 525 aa, 1 stop
<MW: 58416, pI: 6.62, NX(S/T): 1
MECCRATPGTLLLLFLAFLLLSSRTARSEEDRDGLWDAGWPWSECSRTC GGGASYSLRRCLS
SKSCEGRNIRYRTC SNVDCPPEAGDFRAQQCSAHNDVKHHGQFYEWLPVSNPDNPCSLKQC
AKGTTLVVELAPKVLGDGTRCYTESLDMCISGLCQIVGCDHQLGSTVKEDNCGVCNGDGSTCR
LVRGQYKSQLSATKSDDTVVALPYGSRHIRLVKGPDLHLYLETKTLQGTKGENSLSSTGTFL
VDNSSVDFQKFPDKIELRMAGPLTADFIVKIRNSGSADSTVQFIFYQPIIHRWRETDFFPCS
ATCGGGYQLTSAECYDLRSNRVADQYCHYYPENIKPKPKLQECNLDPASDGYKQIMPYD
LYHPLPRWEATPWTACSSSCGGGIQSRVSCVEEDIQGHVTSVEEWKCMYTPKMPIAQPCNI
FDCPKWLAQEWSPCTVTTCGQLRYRVVLCIDHRGMHTGGCSPKTKPHIKEECIVPTPCYKPK
EKLFPVEAKLPWFKQAQEEGA AVSEEPS

Important features:

Signal peptide:

amino acids 1-25

N-glycosylation site.

amino acids 251-254

Thrombospondin 1

amino acids 385-399

von Willebrand factor type C domain proteins

amino acids 385-399, 445-459 and 42-56

FIGURE 121

CGGACGCGTGGGCGGCGGCTGCGGAAGTCCCGTGGAGGGGCCGCTGGGCCCTCGGGCCCTGAC
AGATGGCAGTGGCCACTGCGGCGGCAGTACTGGCCGCTCTGGGCGGGCGCTGTGGCTGGCG
GCCCGCCGTTCTGTTGGGCGCCAGGGTCCAGCGGCTGCGCAGAGCGGGGACCCCGGCTCAT
GCACGGGAAGACTGTGTGATCACCAGGGCGAACAGCGGCCTGGGCGCGGCCAGCGCGCCG
AGCTACTGCGCCTGGGAGCGCGGGTGATCATGGGCTGCCGGGACCGCGCGCGCCGAGGAG
GCGGCGGGTCAGTCCGCGCGAGCTCCGCCAGGCGCGGAGTGCGGCCAGAGCCTGGCGT
CAGCGGGTGGGCGAGCTCATAGTCCGGGAGCTGGACCTCGCCTCGCTGCGCTCGGTGCGCG
CCTTCTGCCAGGAAATGCTCCAGGAAGAGCCTAGGCTGGATGTCTTGATCAATAACGCAGGG
ATCTTCCAGTGCCCTTACATGAAGACTGAAGATGGGTTTGAGATGCAGTTCGGAGTGAACCA
TCTGGGGCACTTTCTACTACCAATCTTCTCCTTGGACTCCTCAAAGTTTCAGCTCCAGCA
GGATTGTGGTAGTTTCTTCCAAACTTTATAAATACGGAGACATCAATTTTGATGACTTGAAC
AGTGAAACAAAGCTATAATAAAAGCTTTTGTTATAGCCGAGCAAACTGGCTAACATTCTTTT
TACCAGGGAACTAGCCCGCGCTTAGAAGGCACAAATGTACCGTCAATGTGTGCATCCTG
GTATTGTACGGACAAATCTGGGGAGGCACATACACTTCCACTGTTGGTCAAACTCTCTT
AATTTGGTGTCTATGGGCTTTTTTCAAACCTCCAGTAGAAGGTGCCAGACTTCCATTTATTT
GGCCTCTTCACTGAGGTAGAAGGAGTGTCCAGGAAGTACTTTGGGGATTGTAAGAGGGAAG
AACTGTTGCCCAAAGCTATGGATGAATCTGTTGCAAGAAAAGCTCTGGGATATCAGTGAAGTG
ATGGTTGGCCTGCTAAAATAGGAAACAAGGAGTAAAAGAGCTGTTTATAAACTGCATATCAG
TTATATCTGTGATCAGGAATGGTGTGGATTGAGAACTTGTTACTTGAAGAAAAAGAAATTTT
ATATTGGAATAGCCTGCTAAGAGGTACATGTGGGTATTTTGGAGTTACTGAAAAATATTTT
TGGGATAAGAGAATTTTCAGCAAAGATGTTTTAAATATATATAGTAAGTATAATGAATAATA
GTACAATGAAAAATACAATTATATTGTAATAATATACTGGGCAAGCATGGATGACATATTA
ATATTGTGAGAATTAAGTGAAGTCAAGTGTATCGAGAGGTTTTTCAAGTATCTTTGAGTT
TCATGGCCAAAGTGTTAACTAGTTTTACTACAATGTTTGGTGTGTTGTGTGGAAATTATCTGC
CTGTTGTGTGCACACAAGTCTTACTTGGAAATAAATTTACTGGTAC

FIGURE 122

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58747
<subunit 1 of 1, 336 aa, 1 stop
<MW: 36865, pI: 9.15, NX(S/T): 2
MAVATAAAVLAAALGGALWLAARRFVGPRVQRLRRGGDPGLMHGKTVLITGANSGLGRATAAE
LLRLGARVIMGCRDRARAEAAAGQLRREL RQAAECGPEPGVSGVGELIVRELDLASLRSVRA
FCQEMLQEEPRLDVLINNAGIFQCPYMKTEDGFEMQFGVNH LGHFLLTNLLGLLKSSAPSR
IVVVSSKLYKYGDINFDDLNSEQSYNKSFCYSRSLANILFTRELARRLEGTNVTVNVLHPG
IVRTNLGRHIHIPLLVKPLFNLVSWAFFKTPVEGAQTSIYLASSPEVEGVSGRYFGDCKEEE
LLPKAMDESVARKLWDISEVMVGLLK

Important features:

Signal peptide:

amino acids 1-21

Short-chain alcohol dehydrogenase family protein

amino acids 134-144, 44-56 and 239-248

N-glycosylation site.

amino acids 212-215 and 239-242

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GGGGATTGTAAGAGAGAAAGNACTGTGCCCAAAGNTATGGATGAATCTGTTGCAAGAAAATTN
TGGGATATCAGTGAAGTGATGTTTNGCCTGCTAAAAATAGGAACAAGGAGTAAAAGAGCTGTT
TATAAAACATGCATATCAGTTATATCTGTGATCAGGAATGGTGTGGATTGAGAACTTGTTACT
TGAAGAAAAAGAATTTTGATATTGGAATAGCCTGNTAAGAGGNCATGTGGGTATTTTGAGAG
TTACTGAAAAATTATTTTGGGATAAGAGAAATTCAGCAAAGATGTTTTAAATATATATAGT
AAGTATAATGAATAATAAGTACAATGAAAAATACAATTTATATTGTAAAAATTATACTGGGCA
AGCATGGATGATCATTAAATTTATTTGTCAGAATTAAGTGACTCAAAGTGCTATCGAGAGGTTT
TTCAGTATCTTTCAGTGTTCATGCGCCAAAGTGTTAACTAGTTTTACTACAATGTTTGGTGT
TTGTGGAATAATTCTGCCTGGCTT

FIGURE 124

GAGAGGACGAGGTGCCGCTGCCTGGAGAATCCTCCGCTGCCGTCGGCTCCCGAGCCAGCC
CTTTCTTAACCCAACCAACCTAGCCAGTCCCAGCCGCGCAGCCCTGTCCCTGTACGGAC
CCCAGCGTTACCATAGCATCCTGCCGCTCTTCTATCCTTACCCGACCTCAGATGCTCCCTTCT
GCTCTGGTAACTTGGGTTTTTACTCCTGTAACAACGAAATAACAAGTCTTGCTACAGAGA
ATATAGATGAAATTTTAAACAATGCTGATGTTGCTTTAGTAAATTTTTATGCTGACTGGTGT
CGTTTCAGTCAGATGTTGCATCCAATTTTTGAGGAAGCTTCCGATGTCAATTAGGAAGAATT
TCCAAATGAAATCAAGTAGTGTGTTGCCAGAGTTGATTGTGATCAGCACTCTGACATAGCCC
AGAGATACAGGATAAGCAAATACCCAACCCCTCAAATGTTTTCGTAATGGGATGATGATGAAG
AGAGAATACAGGGGTGAGCGATCAGTGAAGCATTGGCAGATTACATCAGGCAACAAAAAAG
TGACCCCATTCAGAAATTCGGGACTTAGCAGAAATCACCACCTTTGATCGCAGCAAAAGAA
ATATCATTGGATATTTTGAAGAAAGGACTCGGACAACTATAGAGTTTTTGAACGAGTAGCG
AATATTTTGCATGATGACTGTGCCTTTCTTTCTGCAATTGGGGATGTTTCAAACCGGAAAG
ATATAGTGGCGACAACATAATCTACAACACCAGGGCATTCTGCTCCGATATGGTGTACT
TGGGAGCTATGACAAATTTTATGATGTGACTTACAATTGGATTCAAGATAAATGTTCCCTCTT
GTCCGAGAAATAACATTTGAAATGGAGAGGAATTGACAGAAGAAGGACTGCCTTTTCTCAT
ACTCTTTCACATGAAAGAAGATACAGAAAGTTTAGAAATATCCAGAATGAAGTAGCTCGGC
AATTAATAAGTGAAAAAGGTACAATAAACTTTTACATGCCGATTGTGACAAATTTAGACAT
CCTCTTCTGCACATACAGAAAACCTCCAGCAGATTGTCTGTAATCGCTATTGACAGCTTTAG
GCATATGTATGTGTTTGGAGACTTCAAAGATGTATTAATTCCTGGAAAACCAAGCAATTCTG
TATTTGACTTACATTCTGGAAAACCTGCACAGAGAATTCCATCATGGACCTGACCCAACTGAT
ACAGCCCAGGAGAGCAAGCCCCAAGATGTAGCAAGCAGTCCACCTGAGAGCTCCTTCCAGAA
ACTAGCACCCAGTGAATATAGGTATACTCTATTGAGGGATCGAGATGAGCTTTAAAAAACTTG
AAAAACAGTTTGTAAAGCCTTCAACAGCAGCATCAACCTACGTGGTGGAATATGAAACCTA
TATTTTCATAATTCTATGTGTATTTTATTTTGAATAAACAGAAAGAAATTTAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 125

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57689

<subunit 1 of 1, 406 aa, 1 stop

<MW: 46927, pI: 5.21, NX(S/T): 0

MHPAVFLSLPDLRCSLLLLVTWVFTPVTTEITSLATENIDEILNNADVALVNFYADWCRFSQ
MLHPIFEEASDVIKEEFPNENQVVFARVDCDQHS DIAQRYRISKYPTLKLFRNGMMMKREYR
GQRSVKALADYIRQQKSDPIQEIRDLAEITTLDRSKRNIIGYFEQKSDSNYRVFERVANILH
DDCAFLSAFGDVSKPERYSGDNIIYKPPGHSAPDMVYLGAMTNFDTVYTNWIQDKCVPLVREI
TFENGEEELTEEGLPFLILFHMKEDTESLEIFQNEVARQLISEKGTINFLHADCDKFRHPLLH
IQKTPADCPVIAIDSFHMYVFGDFKDVLI PGKLKQFVFDLHSGKLHREFHHGPDPTDTAPG
EQAQDVASSPPES SFQKLAPSEYRYTLLRDRDEL

Important features:

Signal peptide:

amino acids 1-29

Endoplasmic reticulum targeting sequence.

amino acids 403-406

Tyrosine kinase phosphorylation site.

amino acids 203-211

Thioredoxin family proteins

amino acids 50-66

FIGURE 126

ATTAAGGAAGAATTTCCAAATGAAAATCAAGTAGTNTTTGCCAGAGTNGATTGTGATCAGCA
CTCTGACATAGCCCAGAGATACAGGATAAGCAAATACCCAACCCCTCAAATTGTTTCGTAATG
GGATGATGATGAAGAGAGAATACAGGGGT CAGCGATCAGTGAAAGCATTGGCAGATTA

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FIGURE 127

AGAGGCCTCTCTGGAAGTTGTCCCGGTGTTGCGCCGNGGAGCCCGGGTCGAGAGGACNAGG
TGCCGCTGCCTGGAGAATCCTCCGCTGCCGTGGGCTCCCGGAGCCAGCCCTTTCCTAAGCC
AACCCAACCTAGCCCGTCCAGCCGCCAGCGCCTGTCCCTGTGTCGCGANCCAGCGTNACC
ATGCATCCTGCCGTCTTCCTATCCTTACCCGACCTCAGATGCTCCCTTCTGCTCCTGGTAAC
TTGGGTTTTTACTCCTGTAACAACCTGAAATAACNNGTCTTGATACNNAGAATATAGATGAAA
TTTTAAACNATGCTGATGTGGCTTTAGTCAATTTTTATGCTGACTGGTGTGCTTTCAGTCAG
ATGTGGCATCCAATTTTTGAGGANGCTTCCGATGTCATTAAGGAAGAATTTCCAAATGAAAA
TCAAGTAGTGTGTTGCCAGAGTTGATTGTGATCAGCACTCTGACATAGCCAGAGATACAGGA
TAAGCAAATACCCAACCCCTCAAATTGTTTCGTAATGGGATGATGATGAAGAGAGAATAACAGG
GGTCAGCGATCAGTGAAAGCATTGGCAGATTACATCAGGC

FIGURE 128

GCCCACGCGTCCGATGGCGTTACGTTTCGCGGCCTTCTGCTACATGCTGGCGCTGCTGCTCA
CTGCGCGCTCATCTTCTTCGCCATTGGCACATTATAGCATTGATGAGCTGAAGACTGAT
TACAAGAATCCTATAGACCAGTGTAAATACCCTGAATCCCCCTTGCTACTCCAGAGTACCTCAT
CCACGCTTCTTCTGTGTATGTTCTTGTGTCAGCAGAGTGGCTTACACTGGGTCTCAATA
TGCCCTCTTGGCATATCATATTTGGAGGTATATGAGTAGACCAGTGATGAGTGGCCAGGA
CTCTATGACCCTACAACCATCATGAATGCAGATATTCTAGCATATTGTCAGAAGGAAGGATG
GTGCAAAATTAGCTTTTTATCTTCTAGCATTTTTTTACTACCTATATGGCATGATCTATGTTT
TGGTGAGCTCTTAGAACAACACACAGAAGAATTGGTCCAGTTAAGTGCATGCAAAAAGCCAC
CAAATGAAGGGATTCTATCCAGCAAGATCCTGTCCAAGAGTAGCCTGTGGAATCTGATCAGT
TACTTTAAAAAATGACTCCTTATTTTTTAAATGTTTCCACATTTTGTGTTGTGAAAGACTG
TTTTCATATGTTATACTCAGATAAAGATTTTAAATGGTATTACGTATAAATTAATATAAAAT
GATTACCTCTGGTGTTGACAGGTTTGAAGTTGCACITTCCTAAGGAACAGCCATAATCCTCTG
AATGATGCATTAATTACTGACTGTCCTAGTACATTGGAAGCTTTTGTATTATAGGAACCTTGTA
GGGCTCATTTTGGTTTCATTGAAACAGTATCTAATTATAAATTAGCTGTAGATATCAGGTGC
TTCTGATGAAGTGAAAATGTATATCTGACTAGTGGGAACTTCATGGGTTTCTCATCTGTC
ATGTCGATGATTATATATGGATACATTTACAAAAATAAAAGCGGGAATTTTCCCTTCGCTT
GAATATTATCCCTGTATATTGCATGAATGAGAGATTTCCCATATTTCCATCAGAGTAATAAA
TATACTTGCTTTAATTCTTAAGCATAAGTAAACATGATATAAAAAATATATGCTGAATTACTT
GTGAAGAATGCATTTAAAGCTATTTTAAATGTGTTTTTATTGTGAAGACATTACTTATTAAG
AAATTGGTTATTATGCTTACTGTTCTAATCTGGTGGTAAAGGTATTCTTAAGAATTGTCAGG
TACTACAGATTTTCAAACCTGAATGAGAGAAAATTGTATAACCATCCTGCTGTTCTCTTAGT
GCAATACAATAAAACTCTGAAATTAAGACTC

FIGURE 129

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA23330

<subunit 1 of 1, 144 aa, 1 stop

<MW: 16699, pI: 5.60, NX(S/T): 0

MAFTFAAFCYMLALLLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHAFF
CVMFLCAAEWLTGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGWCKLA
FYLLAFFYYLYGMIYVLVSS

Important features:

Signal peptide:

amino acids 1-20

Type II transmembrane domain:

amino acids 11-31

Other transmembrane domain:

amino acids 57-77 and 123-143

FIGURE 130

ATTATAGCATTTGATGAGCTGAAGACTGATTACAAGATCCTATAGACCAGTGTAATACCCTG
AATCCCCCTTGTA C TCCAGAGTACCTCATCCACGCTTTCTTCTGTGCATGTTTCTTTGTGC
AGCAGAGTGGCTTACACTGGGTCTCAATATGCCCCCTCTTGGCATATCATATTTGGAGGTATA
TGAGTAGACCAGTGATGAGTGGCCCAGGACTCTATGACCCCTACAACCATCATGAATGCAGAT
ATTCTAGCATATTGT CAGAAGGAAGGATGGTGCAAATTAGCTTTTTATCTTCTAGCATTTTT
TTACTACCTATATGGCATGATCTATGTTTTGGTGAGCTCTTAGAACAACACAGAAGAATT
GGTCCAGTTAAGTG CATGCAAAAAGCCACCAAATGAAGGGATTCTATCCAGCAAGATCCTGT
CCAAGAGTAGCCTGTGGAATCTGATCAGTTACTTTAAAAAATG

FIGURE 131

CGGACGCGTGGGGGAAACCCCTCCGAGAAAACAGCAACAAGCTGAGCTGCTGTGACAGAGGG
GAACAAGATGGCGGCGCCGAAGGGGAGCCTCTGGGTGAGGACCCAACTGGGGCTCCCGCCGC
TGCTGCTGCTGACCATGGCCTTGGCCGGAGGTTGCGGGACCGCTTCGGCTGAAGCATTTGAC
TCGGTCTTGGGTGATACGGCGTCTTGCCACCGGGCCTGTCAAGTTGACCTACCCCTTGACAC
CTACCCTAAGGAAGAGGAGTTGTACGCATGTCAGAGAGGTTGCAGGCTGTTTTCAATTTGTC
AGTTTGTGGATGATGGAATTGACTTAAATCGAACTAAATGGAATGTGAATCTGCATGTACA
GAAGCATATTTCCCAATCTGATGAGCAATATGCTTGCCATCTTGGTTGCCAGAATCAGCTGCC
ATTCGCTGAACTGAGACAAGAACAACCTTATGTCCCTGATGCCAAAAATGCACCTACTCTTTC
CTCTAACTCTGGTGAGGTCATTCTGGAGTGACATGATGGACTCCGCACAGAGCTTCATAACC
TCTTCATGGACTTTTTATCTTCAAGCCGATGACGGAAAAATAGTTATATTCAGTCTAAGCC
AGAAATCCAGTACGCACCACATTTGGAGCAGGAGCCTACAAATTTGAGAGAATCATCTCTAA
GCAAAATGTCTTATCTGCAATGAGAAATTCACAAGCGCACAGGAATTTTCTTGAAGATGGA
GAAAGTGATGGCTTTTAAAGATGCCTCTCTTAACTCTGGGTGGATTTTAACTACAACCTCT
TGTCTCTCGGTGATGGTATTGCTTTGGATTTGTTGTGCAACTGTTGCTACAGCTGTGGAGC
AGTATGTTCCCTCTGAGAAGCTGAGTATCTATGGTGACTTGGAGTTTATGAATGAACAAAAG
CTAAACAGATATCCAGCTTCTTCTTGTGGTTGTTAGATCTAAAACCTGAAGATCATGAAGA
AGCAGGGCCTCTACCTACAAAAGTGAATCTTGCTCATTCTGAATTTAAGCATTTTTCTTTT
AAAAGACAAGTGTAATAGACATCTAAAATCCACTCCTCATAGAGCTTTTAAAATGGTTTCA
TTGGATATAGGCCTTAAGAAATCACTATAAAATGCAAATAAGTTACTCAATCTGTG

FIGURE 132

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA26847

<subunit 1 of 1, 323 aa, 1 stop

<MW: 36223, pI: 5.06, NX(S/T): 1

MAAPKGSLWVRTQLGLPPLLLLLTALAGGSGTASAEAFDSVLGDTASCHRAQQLTYPLHTYP
KEEELYACQRCRLFSICQFVDDGIDLNRKLECESACTEAYSQSDEQYACHLGCQNQLPFA
ELRQEQLMSLMPKMHLLFPLTLVRSFWSMMDSAQSFITSSWTFYLQADDGKIVIFQSKPEI
QYAPHLEQEPTNLRESSLSKMSYLQMRNSQAHRNFLEDGESDGFLRCLSLNSGWILTTLVL
SVMVLLWICCATVATAVEQYVPSEKLSIYGDLEFMNEQKLNRYPASSLVVVRSKTEDHEEAG
PLPTKVNLAHSEI

Important features:

Signal peptide:

amino acids 1-31

Transmembrane domain:

amino acids 241-260

N-glycosylation site.

amino acids 90-93

FIGURE 133

TTGGGTGATACGGCGTCTTGCCACCGGGCCTGTCAGTTGACCTACCCCTTGCACACCTACCC
TAAGGAAGAGGAGTTGTACGCATGTCAGAGAGGTTGCAGGCTGTTTTCAATTTGTCAGTTTG
TGGATGATGGAATTGACTTAAATCGAACTAAATTGGAAATGTGAATCTGCATGTACAGAAGCA
TATTCCCAATCTGATGAGCAATATGCTTGCCATCTTGGTTGCCAGAATCAGCTGCCATTTCGC
TGAAGTGAAGACAAGAACAACCTTATGTCCCTGATGCCAAAATGCACCTACTCTTTCCTCTAA
CTCTGGTGAGGTCATTCTGGAGTGACATGATGGACTCCGC

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FIGURE 134

CACACTGGCCGGATCTTTTAGAGTCCTTTGACCTTGACCAAGGGTCNGGAAAAACAGCAACAA
GCTGAGCTGCTGTGACAGAGGGAACAAGATGGCGGCCCGAAGGGAGCCTTTGGGTGAGGAC
CCAACTGGGGCTCCCGCCGCTGCTGCTGCTGACCATGGCCTTGGCCGGAGGTTTCGGGGACCG
CTTCGGCTGAAGCATTTGACTCGGTCTTGGGTGATACGGCGTCTTGCCACCGGGCCTGTCAG
TTGACCTACCCCTTGACACCTACCCTAAGGAAGAGGAGTTGTACGCATGTCAGAGAGGTTG
CAGGCTGTTTTCAATTTGTGAGTTTGTGGATGATGGAATTGACTTAAATCGAACTAAATTGG
AATGTGAATCTGCATGTACAGAAGCATATTCCTAATCTGATGAGCAATATGCTTGCCATCTT
GGTTGCCAGAATCAGCTGCCATTGCTGAACTGAGACAAGAACAACCTTATGTCCCTGATGCC
AAAAATGCACCTACTCTTCTCTAACTCTGGTGAGGTCACTCTGGAGTGACATGATGGACT
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FIGURE 135

GCAGAGTGGCGATCGCTGAGAGGCAGGAGGGCCGAGGCGGGCCTGGGAGGCGGCCCGGAGGT
GGGGCGCCGCTGGGGCCGGCCCGCACGGGCTTCATCTGAGGGCGCACGGCCCCGACCGAGC
GTGCGGACTGGCCTCCCAAGCGTGGGGCGACAAGCTGCCGGAGCTGCAATGGGCGCGGCTG
GGGATTCTGTCTGGCCTCCTGGGCGCCGTGTGGCTGCTCAGCTCGGGCCACGGAGAGGAGC
AGCCCCCGGAGACAGCGGCACAGAGGTGCTTCTGCCAGGTTAGTGGTTACTTGGATGATTGT
ACCTGTGATGTTGAAACCATTGATAGATTTAATAACTACAGGCTTTTCCCAAGACTACAAAA
ACTTCTTGAAAGTGACTACTTTAGGTATTACAAGGTAAACCTGAAGAGGCCGTGTCTTTCT
GGAATGACATCAGCCAGTGTGGAAGAAGGACTGTGCTGTCAAACCATGTCAATCTGATGAA
GTTCTGTATGGAATTAATCTGCGAGCTACAAGTATTCTGAAGAAGCCAATAATCTCATTGA
AGAATGTGAACAAGCTGAACGACTTGGAGCAGTGGATGAATCTCTGAGTGAGGAAACACAGA
AGGCTGTTCTTCACTGGACCAAGCATGATGATTCTTCAGATAACTTCTGTGAAGCTGATGAC
ATTCACTCCCTGAAGCTGAATATGTAGATTGCTTCTTAATCCTGAGCGCTACACTGGTTA
CAAGGGACCAGATGCTTGGAAAAATATGGAATGTCACTACGAAGAAAAGCTGTTTTAAGCCAC
AGACAATTAAGACCTTTAAATCCTTTGGCTTCTGGTCAAGGGACAAGTGAAGAGAACACT
TTTTACAGTTGGCTAGAAGGTCTCTGTGTAGAAAAAGAGCATTCTACAGACTTATATCTGG
CCTACATGCAAGCATTAAATGTGCATTTGAGTGCAAGATATCTTTTACAAGAGACCTGGTTAG
AAAAGAAATGGGGACACAACATTACAGAATTTCAACAGCGATTTGATGGAATTTTGACTGAA
GGAGAAGGTCCAAGAAGGCTTAAGAACTTGTATTTTCTCTACTTAATAGAATAAGGGCTTT
ATCCAAAGTGTTACCATTTCTCGAGCGCCAGATTTTCAACTCTTTACTGGAATAAAAATTC
AGGATGAGGAAAAAAAATGTTACTTCTGGAATACTTCATGAAATCAAGTCATTTCTTTG
CATTTTGATGAGAATTCATTTTTGCTGGGGATAAAAAAGAAGCACAACTAAAGGAGGA
CTTTGCACTGCATTTTAGAAATATTTCAAGAATTATGGATTGTGTTGGTTGTTTTAAATGTC
GTCTGTGGGAAAGCTTCAGACTCAGGGTTTGGGCACTGCTCTGAAGATCTTATTTTCTGAG
AAATGTATAGCAAATATGCCAGAAAAGTGGACCTAGTTATGAATTCATCTAACAGACAAGA
AATAGTATCATTATCAACGCATTTGGAAGAATTTCTACAAGTGTGAAGAATTAGAAAAT
TCAGGAACCTGTTACAGAATATTCATTAAAGAAAAACAAGCTGATATGTGCCGTGTTCTGGAC
AATGGAGGCGAAAGAGTGGAAATTCATTCAAAGGCATAATAGCAATGACAGTCTTAAGCCAA
ACATTTTATATAAAGTTGCTTTTGTAAAGGAGAATTATATTGTTTTAAGTAAACACATTTTT
AAAAATGTGTAAAGTCTATGTATAATACTACTGTGAGTAAAGTAATACTTTAATAATGTG
GTACAAATTTTAAAGTTTAATATGAATAAAAGGAGGATTATCAAATTAATAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 136

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53974
<subunit 1 of 1, 468 aa, 1 stop
<MW: 54393, pI: 5.63, NX(S/T): 2
MGRGWGFLFGLLGAVWLLSSGHGEEQPPETAAQRCFCQVSGYLDCTCDVETIDRFNNYRLF
PRLQKLLESDFRYYKVNLRPCPFWNDISQCGRDCAVKPCQSDEVDPDGIKSASYKYSEEA
NNLIEECEQAERLGAVDESLSSETQKAVLQWTKHDDSSDNFCEADDIQSPEAEYVDLLLNP
RYTGYKGPDAWKIWNVIYEENCFKPQTIKRPLNPLASGQGTSEENTFYSWLEGLCVEKRAFY
RLISGLHASINVHLSARYLLQETWLEKKWGHNITEFQQRFDGILTEGEGPRRLKNLYFLYLI
ELRALSKVLFFFERPDFQLFTGNKIQDEENKMLLLEILHEIKSFPLHFDENSFFAGDKKEAH
KLKEDFRLHFRNISRIMDCVGCFCRLWGKLQTQGLGTALKILFSEKLIANMPESGPSYEFH
LTRQEIVSLFNAFGRISTSVKELENFRNLLQNIH

Important features:

Signal peptide:

amino acids 1-23

N-glycosylation site.

amino acids 280-283 and 384-387

Amidation site.

amino acids 94-97

Glycosaminoglycan attachment site.

amino acids 20-23 and 223-226

Aminotransferases class-V pyridoxal-phosphate

amino acids 216-222

Interleukin-7 proteins

amino acids 338-343

FIGURE 137

GCTGGAAATATGGATGTCATCTACGAGAACTGTTTTAAGCCACAGACAATTAAAAGACCTT
TAAATCCTTTGGCTTCTGGTCAAGGGACAAGTGAAGAGNACACTTTTTACAGTTGGCTAGAA
GGTCTCTGTGTAGAAAAAGAGCATTCTACAGACTTATATCTGGCCTACATGCAAGCATTAA
TGTGCATTTGAGTGCAAGATATCTTTACAAGAGACCTGGTTAGAAAAGAAATGGGGACACA
ACATTACAGAATTTNACAGCGATTTGATGGAATTTTGACTGAAGGAGAAGGTCCAAGAAGG
CTTAAGAACTTGTATTTCTCTACTTAATAGAACTAAGGGCTTTATCCAAAGTGTTACCATT
CTTNGAGCGCCAGATTTTCAACTNNTTTACTGGAAATAAAATTCAGGATGAGGNAAACAAA
TGTTACTTTTGGAATACTTCATGAAATCAAGTCATTTCTTTGCATTTTGATGAGAATCA
TTTTTTTGCTG

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FIGURE 138

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGTTGGGAGGGGGCAGGATGGGAGGGAA
AGTGAAGAAAAACAGAAAAGGAGAGGGACAGAGGCCAGGACTTCTCATACTGGACAGAAAC
CGATCAGGCATGGAACTCCCCTTCGTCACCTCACTGTTCTTGCCTCGTGTTCCTGACAGG
TCTCTGCTCCCCCTTTAACCTGGATGAACATCACCCACGCTATTCCCAGGGCCACCAGAAG
CTGAATTGGATACAGTGTCTTACAACATGTTGGGGGTGGACAGCGATGGATGCTGTGTGGGC
GCCCCCTGGGATGGGCCTTCAGGCGACCGGAGGGGGGACGTTTATCGTGCCTCTGAGGGGG
GGCCCCAATGCCCCATGTGCCAAGGGCCACTTAGGTGACTACCAACTGGGAAATTCTATCTC
ATCCTGCTGTGAATATGCACCTGGGGATGTCTCTGTTAGAGACAGATGGTGATGGGGGATTC
ATGGTGAGCTAAGGAGAGGGTGGTGGCAGTGTCTCTGAAGGTCCATAAAAGAAAAAGAGAA
GTGTGGTAAGGGAAAATGGTCTGTGTGGAGGGGTCAAGGAGTTAAAAACCTAGAAAAGCAAA
AGGTAGGTAAATGTCAGGGAGTAGTCTTCATGCCTCCTCAACTGGGAGCATGTTCTGAGGGT
GCCCTCCCAAGCCTGGGAGTAAGTATTTCCCCATCCCCAGGCCTGTGCCCTCTCTGGTCT
CGTGCTTGTGGCAGCTCTGTCTTCAGTTCCTGGGATATGTGCCCGTGTGGATGCTTCATTCCA
GCCTCAGGAAGCCTGGCACCCATGCCCCAACGTGAGCCAGAGGAAGGCTGAGTACTTGGTIT
CCCAGAAGGAGATACTGGGTGGGAAAAAGATGGGGCAAGCGGTATGATGCCCTGGCAAGGG
CCTGCATGGCTATCCTCATTGCTACCTAATGTGCTTGC AAAAGCTCCATGTTTCCTAACAGA
TTCAGACTCCTGGCCAGGTGTGGTGGCCCCACCTGTAATTCTAGCACTTGGGAGGCCAAG
GTGGGCAGATCACTTGAGGTGAGGAGTTCAAGACCAGCCTGGCCAAACATGGTGAAACTCCAT
CTCTACTAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA
ATCTACTCGGGAGGCTAAGACAGGAGACTCTCACTTCAACCCAGGAGGTGAGGTTGCGGTG
AGCCAAGATTGTGCCTCTGCACTTAGCGTGGGTGACAGAGTAAGCGAGACTCCATCTCAAA
AATAATAATAATAATAAATTCAGACTCCTTATCAGGAGTCCATGATCTGGCCTGGCACAGTAA
CTCATGCCTGTAATCCCAACATTTTGGGAGGCCAACGCAGGAGGATTGCTTGAAGTCTGGAG
GTTTGAGACCAGCCTGGGCAACATAGAAAAGACCCCATCTCTAAATAAATGTTTTAAAAAT

FIGURE 139

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57039

><subunit 1 of 1, 124 aa, 1 stop

><MW: 13352, pI: 5.99, NX(S/T): 1

MELPFVTHLFLPLVFLTGLCSPFNLDEHHPRLFPGPPEAEFGYSVLQHVGGQRWMLVGAPW
DGPSGDRRGDVYRCVPVGAHNAPCAKGHLGDYQLGNSSHPAVNMHLGMSLLETGDGGGFMVS

Important features:

Signal peptide:

amino acids 1-22

Cell attachment sequence.

amino acids 70-73

N-glycosylation site.

amino acids 98-101

Integrins alpha chain proteins

amino acids 67-81

FIGURE 140

CACAGTTCCCCACCATCACTCNTCCCATTCCTTCCAACTTTATTTTATAGCTTGCCATTGGGA
GGGGGCAGGATGGGAGGGAAAGTGAAGAAAACAGAAAAGGAGAGGGACAGAGGCCAGAGGAC
TTCTCATACTGGACAGAAACGATCAGGCATGGAACCTCCCTTCGTCACTCACCTGTTCTTG
CCCCTGGTGTTCTTGACAGGTCTCTGCTCCCCCTTTAACCTGGATGAACATCACCCACGCCT
ATTCCCAGGGCCACCAGAAGCTGAATTTGGGATACAGTGTCTTACAACATGTTGGGGGTGGAC
AGCGATGGATGCTGGTGGGCGCCCCCTGGGATGGGCCTTCAGGCGACCGGAGGGGGGACGTT
TATCGCTGCCCTGTAGGGGGGGCCCAATGCCCCATGTGCCAAGGGCCACTTAGGTGACTA
CCAACTGGGAAATTCATCTCATCCTGCTGTGAATATGCACCTGGGGATGTCTCTGTTAGAGA
CAGATGGTGATGG

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FIGURE 141

AAAGTTACATTTTCTCTGGAACCTCCTAGGCCACTCCCTGCTGATGCAACATCTGGGTTTG
GGCAGAAAGGAGGGTGCTTCGGAGCCCGCCCTTTCTGAGCTTCCTGGGCCGGCTCTAGAACA
ATTACGGCTTCGCTGCGACTCAGACCTCAGCTCCAACATATGCATTCTGAAGAAAGATGGCT
GAGATGGACAGAATGCTTTATTTTGGAAAGAAACAATGTTCTAGGTCAAACCTGAGTCTACCA
AATGCAGACTTTCCAAATGTTTCTAGAAGAAATCTGGACAAGTCTTTTCATGTGGTTTTTCT
ACGCATTGATTCATGTTTGGCTCACAGATGAAGTGGCCATTCTGCCTGCCCTCAGAACCTC
TCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCAGTGATCGCGCTGGAGA
AACAGTGTACTATTCTGTGCAATACCAGGGGGAGTACGAGAGCCTGTACACGAGCCACATCT
GGATCCCAGCAGCTGGTGCTCACTCACTGAAGGTCTGAGTGTGATGTCATGTGATGACATC
ACGGCCACTGTGCCATACAACCTTCGTGTCAGGGCCACATTGGGCTCACAGACCTCAGCCTG
GAGCATCCTGAAGCATCCCTTTAATAGAACTCAACCATCCTTACCCGACCTGGGATGGAGA
TCACCAAAGATGGCTTCCACCTGGTTATTGAGCTGGAGGACCTGGGGCCCAAGTTTGAGTTC
CTTGTGGCCTACTGGAGGAGGGAGCCTGGTGCCGAGGAACATGTCAAATGGTGAGGAGTGG
GGGTATTCCAGTGCACCTAGAAACCATGGAGCCAGGGGCTGCATACTGTGTGAAGGCCCAGA
CATTGCTGAAGGCCATTGGGAGGTACAGCGCCTTCAGCCAGACAGAATGTGTGGAGGTGCAA
GGAGAGGCCATTCCCTGGTACTGGCCCTGTTTGCCCTTGTGTGGCTTCATGCTGATCCTTGT
GGTGTGCCACTGTTCTGCTGGAATAATGGGCCGGCTGCTCCAGTACTCCTGTTGCCCGGTGG
TGGTCTCTCCAGACACTTTGAAAATAACCAATTCACCCAGAAAGTTAATCAGCTGCAGAAGG
GAGGAGGTGGATGCTGTGCCACGGCTGTGATGTCTCCTGAGGAACCTCCTCAGGGCCTGGAT
CTCATAGGTTTTGCGGAAGGGCCAGGTGAAGCCGAGAACCTGGTGTGCATGACATGGAACCC
ATGAGGGGACAAGTTGTGTTTCTGTTTTCCGCCACGGACAAGGGATGAGAGAAGTAGGAAGA
GCCGTGTTGTCTACAAGTCTAGAAGCAACCATCAGAGGCAGGGTGGTTTGTCTAACAGAACAC
TGACTGAGGCTTAGGGGATGTGACCTCTAGACTGGGGGCTGCCACTTGCTGGCTGAGCAACC
CTGGGAAAAGTGACTTCATCCCTTCGGTCTTAAGTTTCTCATCTGTAATGGGGGAATTACC
TACACACCTGCTAAACACACACACAGAGTCTCTCTATATATACACAGTACACATAAA
TACACCCAGCACTTGCAAGGCTAGAGGGAAACTGGTGACACTCTACAGTCTGACTGATTTCAG
TGTTCCTGGAGAGCAGGACATAAATGTATGATGAGAATGATCAAGGACTCTACACACTGGGT
GGCTTGGAGAGCCCACTTTCCCGAATAATCCTTGAGAGAAAAGGAATCATGGGAGCAATGG
TGTGAGTTCACTTCAAGCCCAATGCCCGTGACAGGGGAATGGCTTAGCGAGCTCTACAGT
AGGTGACCTGGAGGAAGGTACAGCCACACTGAAAATGGGATGTGCATGAACACGGAGGATC
CATGAACTACTGTAAGTGTGACAGTGTGTGCACACTGCAGACAGCAGGTGAAATGTATGT
GTGCAATGCGACGAGAATGCAGAAGTCAGTAACATGTGCATGTTTGTGTGCTCCTTTTTTC
TGTGGTAAAGTACAGAATTACGAAATAAAAGGGCCACCCTGGCCAAAAGCGGTAAAAAA
AAAAA

FIGURE 142

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57033

<subunit 1 of 1, 311 aa, 1 stop

<MW: 35076, pI: 5.04, NX(S/T): 2

MQTFMTVLEEIIWTSLFMWFFYALIPCLLTDEVAILPAPQNL SVLSTNMKHL LMWSPVIA
PGETVYYSVEYQGEYESLYTSHIWI PSSWCSLTEGPEC DVTDDITATVPYNLRVRATLGSQTS
AWSILKHPFNRNSTILTRPGMEITKDG FHLVIELEDLGPQFEFLVAYWRREP GAEEHV
KMVRSGGIPVHLETMEPGAAYCVKAQTFVKAIGRYSAFSQTEC VEVQGEAIPLV
LALFAFVGFM LILVVVPLFVWKMGRL LQYSCCPVVVLPDTLKITNSPQKLISCRREEVD
ACATAVMSPEELLRAWIS

Important features:

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 230-255

N-glycosylation site.

amino acids 40-43 and 134-137

Tissue factor proteins.

amino acids 92-119

Integrins alpha chain proteins

amino acids 232-262

FIGURE 143

TCCTGCTGATGCACATCTGGGTTTGGCAAAGGAGGTTGCTTCGAGCCGCCCTTTCTAGCTT
CCTGGCCGGCTCTAGAACAATTCAGGCTTCGCTGCGACTAGACCTCAGCTCCAACATATGCA
TTCTGAAGAAAGATGGCTGAGATGACAGAATGCTTTATTTTGGAAAGAAACAATGTTCTAGG
TCAAACCTGAGTCTACCAAATGCAGACTTTCACAATGGTTCTAGAAGAAATCTGGACAAGTCT
TTTCATGTGGTTTTTCTACGCATTGATTCCATGTTTGCTCACAGATGAAGTGGCCATTCTGC
CTGCCCTCAGAACCTCTCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCCA
GTGATCGCGCCTGGAGAAAAGTGTACTATTCTGTGGAATACCAGGGGAGTACGAGAGCCT
GTACACGAGCCACATCTGGATCCCAGCAGCTGGTGCTCACTCACTGAAGTCCCTGAGTGTG
ATGTCACTGATGACATCAGGCCACTGTGCCATACAACCTTTGTGTGAGGGCCACATTGGGC
TCACAGACCTCAGCCTGGAGCATCCTGAAGCATCCCTTTAATAGAAACTCAACCATCCTTAC
CCGACCTGGGATGGAGATCACCAAAGATGGCTTNCACCTGGTTATTGAGCTGGAGGACCTGG
GGCCCCAGTTTGAGTTCCTTGTGGCCTANTGGAGGAGGGGCGAACCCCTTGCGCGCAAGGG
GT'T'NGCGAACCCCTTGCGGCCGTGGGGTATCTCTCGAGAAAAGAGAGGCCCAATATGACCC
ACATACTCAATATGGACGAANTGCTATTGTCCACCTGTTTGAGTGGCGCTGGGTTGAT

FIGURE 144

CCCACGCGTCCGCCACGCGTCCGAGGGACAAGAGAGAAGAGAGACTGAAACAGGGAGAAGA
GGCAGGAGAGGAGGAGGTGGGGAGAGCAGAAAGCTGGAGGCCGACACTGAGGGAGGGCGGGA
GGAGGTGAAGAAGGAGAGAGGGGAGAAGAGGCAGGAGCTGGAAGGAGAGAGGGAGGAGGAG
GAGGAGATGCGGGATGGAGACCTGGAGTTAGGTGGCTTGGGAGAGCTTAATGAAAAGAGAAC
GGAGAGGAGGTGTGGTTAGGAACCAAGAGGTAGCCCTGTGGGCAGCAGAAGGCTGAGAGGA
GTAGGAAGATCAGGAGCTAGAGGGAGACTGGAGGGTTCGGGAAAAGAGCAGAGGAAAGAGG
AAAGACACAGAGAGACGGGAGAGAGAAGAAGAGTGGGTTTGAAGGGCGGATCTCAGTCCCTG
GCTGCTTTGGCATTGCGGAACTGGGACTCCCTGTGGGGAGGAGAGGAAAGCTGGAAGTCCT
GGAGGGACAGGGTCCAGAAAGGAGGGACAGAGGAGCTGAGAGAGGGGGCAGGGCGTTGGG
CAGGGGTCCCTCGGAGGCTCCTGGGGATGGGGGCTGCAGCTCGTCTGAGCGCCCCCTCGAGC
GCTGGTACTCTGGGCTGCACTGGGGGCAGCAGCTCACATCGGACCAGCACCTGACCCCGAGG
ACTGGTGGAGCTACAAGGATAATCTCCAGGGAACTTCGTGCCAGGGCCTCCTTTCTGGGGC
CTGGTGAATGCAGCGTGGAGTCTGTGTGCTGTGGGGAAGCGGCAGAGCCCCGTGGATGTGGA
GCTGAAGAGGGTTCTTTATGACCCCTTTCTGCCCCATTAAAGGCTCAGCACTGGAGGAGAGA
AGCTCCGGGGAACTTGTACAACACCGGCCGACATGTCTCCTTCTGCCTGCACCCCGACCT
GTGGTCAATGTGTCTGGAGGTCCCTCCTTTACAGCCACCGACTCAGTGAAGTGGGGTGCT
GTTTGGAGCTCGCGACGGAGCCGGCTCGGAACATCAGATCAACCACAGGGGCTTCTGTCTG
AGGTGCAGCTCATTCACTTCAACCAGGAATCTACGGGAATTTACGCGCTGCCTCCCGCGGC
CCCAATGGCCTGGCCATTCTCAGCCTCTTTGTCAACGTTGCCAGTACCTCTAACCCATTCTC
CAGTCGCCTCCTTAACCGCGACACCATCACTCGCATCTCCTACAAGAATGATGCCCTACTTTC
TTCAAGACCTGAGCCTGGAGCTCCTGTTCCCTGAATCCTTCGGCTTCATCACCTATCAGGGC
TCTCTCAGCACCCCGCCCTGCTCCGAGACTGTCACCTGGATCCTCATTTGACCGGGCCCTCAA
TATCACCTCCCTTCAGATGCATCCCTGAGACTCCTGAGCCAGAATCCTCCATCTCAGATCT
TCCAGAGCCTCAGCGGTAAACAGCCGGCCCTGCGAGCCCTTGGCCACAGGGCACTGAGGGGC
AACAGGGACCCCGGCACCCGAGAGGCGCTGCCAGGCCCAACTACCGCTGCATGTGGA
TGGTGTCCCCCATGTCGCTGAGACTCCCTTCGAGGATTGACCCCGCCGTCTAAGCCTC
CCCACAAGGCGAGGGGAGTTACCCCTAAACCAAAGCTATTAAAGGGACAGAATACTTA

FIGURE 145

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA34353

<subunit 1 of 1, 328 aa, 1 stop

<MW: 36238, pI: 9.90, NX(S/T): 3

MGAAARLSAPRALVLWALGAAAHIGPAPDPEDWWSYKDNLQGNFVPGPPFWGLVNAAWSLC
AVGKRQSPVDVELKRVLYDPFLPPLRLSTGGEKLRGTLINTGRHVSFLPAPRPVVNVSGGPL
LYSHRLSELRLLFGARDGAGSEHQINHQGFSAEVQLIHFNQELYGNFSAASRGPNGLAILSL
FVNVASTSNPFLSRLLNRDTITRISYKNDAFLQDLSLELLFPESFGFITYQGSLSSTPPCSE
TVTWTILIDRALNITSLQMHSRLRLSQNPFSQIFQSLSGNSRPLQLAHRALRGNRDRHPER
RCRGPNYRLHVDGVPHGR

Important features:

Signal peptide:

amino acids 1-23

Transmembrane domain:

amino acids 177-199

N-glycosylation site.

amino acids 118-121, 170-173 and 260-263

Eukaryotic-type carbonic anhydrases proteins

amino acids 222-270, 128-164 and 45-92

FIGURE 146

GGCGCGTGGTTCTGCGGTA CTGGCTGTACGGAGCAGGAGCAAGAGGTGCGCCGCAGCCTCGCCGCGGAGCCTC
GTTCTGTGTCCTCCCGCCCTCGCTCTCGCAGTACTGCTCAGAAACGCTGGGCGCCGCCACCTCGGCAGAGCTAACGAA
GCAGCTCCCTCCCAACCCCACTGCGAGGTCTAATTTTGGACGCTTTGCTGCCATTTCTTCAGGTTTGAGGGAGC
CGCAGAGCGGGAGGCTCGGCTATTCTGCTAGTCAGCACCACGCTCGCCCCCGGACGCTCGGTGCTCAGGCCCTTC
GCGAGCGGGGCTCTCGTCTGCGGTCTCTGTGAAGGCTCTGGCGCGTGCAGAGSCGCGCGCTCGGTTTGGCT
CACCTCTCCAGGAACTTCACTACTGGAGAGCCAAAGAGAGTGGAAAGAGCTGTCTTGAGAGTTTCTCTGGGGAA
ATCCTGAGGTCAATCATTATGAGTGTACCGCGCGGAGTGGCTCAGAGTAACCAAGTGTCTGTTCATGGCTAGA
GCAATPCCAGCCATGTTGGTGTCCCAATGCCACTTTATTGGAGAACTTTTGAAATAATCATGGATGAGGATGGT
GAGTGTGTGCTAGCTGTATCTCCAAACGCTCTAATATGGAGTATATGACATGGATGTAGAGCTGGAAAGA
TCTGCAAGATCCTGGGCTGAAAGTTGCTGTGTGGAAACATGGACCTGCAAGCTTGCTTCCATCAATTGGACAGAAT
TTGGGAGCACACTGGGGAAGATATAGGCCCCCGACGTTTCTGTCACAACTCGTGGTATGATGAAGTGAAGACTTT
AGCTACCCATATGAACATGAATGCAACCCATATTGTCCATTCAGGTGTTCTGGCCCTGTATGTACACATTATACA
CAGGTCTGTGTGGGCACTAGTAAACAGAATCGGTTGTGCCATTAAATTTGTGTATACATGAACATCTGGGGGCGAG
ATATGGCCCAAAGCTGTCTACCTGGTGTGCAATTACTCCCCAAGGGGAACTGGTGGGGCCATGCCCTTACAAA
CATGGGCGGCCCTGTTCTGCTTGCCACCTAGTTTGGAGGGGGCTGTAGAGAAAATCTGTGCTACAAAGAAAGGG
TCAGACAGTATTATCCCCCTCGAAGAGGAGAAACAAATGAATAGAACAGCAGCAGTCAAGTCCATGACACC
CATGTCCGGACAAAGATCAGATGATAGTAGCAGAAATGAAGTATAAGCGCACAGCAAATGTCCCAAATTTGTTTCT
TGTGAAGTAAGATTAAAGAGTCAGTGCAAGGAAACAACTGCAATAGGTACGATGCTCTGCTGGCTGTTTGGAT
AGTAAAGCTAAAGTTATTGGCAGTGATCATTTATGAAATGCAATCCAGCATCTGTAGAGCTGCAATTCATTATGGT
ATAATAGACAAATGATGGTGGCTGGGTAGATACACTAGACAAAGGAAGAAAGCATTATTCATCAAGTCCAAATAGA
AATGGTATTCAAACAAATGGCAAATATCAGTCTGCTAATTCCTTCAAGTCTTAAAGTAACAGTCCAGGCTGTG
ACTTGTGAAACAACTGTGGAACAGCTCTGTCCATTTCATAAGCCTGCTTCAATATGGCCAAAGAGTATACCTGCTC
CGTAACTGTATGCAAGCAAATCCACATTATGCTCGTGTAAATGGAACTCGAGTCTTATCTGATCTGTCCAGTATC
TGCAGAGCAGCAGTACATGCTGGAGTGGTTCGAAATCAAGGTGGTATGTTGATGTAAATGCTGTGGACAAAGA
AAGACCTACATTGCTTCTTTTCAAGATGGAATCTTCTCAGAAAGTTTACAGAACTCTCAGGAGGAAAGGCATTG
AGAGTGTGCTGTGTGTGTAAGTGAATACTTGGAAAGAGACCTAAAGACTATTCCAAATGCAATATTTCTGA
ATTTTGTATAAACTGTAACTACTGTATACAGAGTACATCAACTATTTTTCAGCCCAAAAGGTGCCAAATGCATA
TAAATCTGTATAAACAAAGTCTATATAAATAAAACATGGGACATTAGCTTTGGGAAAAGTAATGAAAATATAATGG
TTTTAGAAATCCGTGTGTTATAATATGCTATATTTCTTAGCAGTTATTTCTACAGTTAATATCATAGTCATGATT
GTTCTACGTTTCATATATTATATGGTCTTTGTATATGCGCACTAATAAAATGAATCTAAACATTGAATGTGAATG
GCCCTCAGAAAATCATCTAGTGCATTTAAATAATATCGACTCTAAACTGAAAGAAACCTTATCACATTTTCCCC
AGTTCAATGCTATGCCATTACCACTCCAAATAATCTCAATAATTTTTCACCTTAATAACTGTAAAGTTTTTTC
TGTAAATCTAGCATAGAAATATAAATCTGATATTGCACTTCTTATTTATATAAAATAATCCCTTAAATATC
CAAATGAATCTGTATAAAATGTTTCTTGTATCTCGGCAAACTACTCTCAGGCCAGGAAGTATAATAGCAAAAAGTT
GAACAAAGATGAACATAATGTATTACATTACCATGGCCATGATTTTTTTTAAATGGTAAATGACCTTGATATATA
ATAATGCGCATATCGGTAACCTATAATGGTGATATATTTGTTTCTATGAAAATGATTTGTGCTTGATACATAA
AATCTGTAAATGTTAGTTTTGGTAATTTTTTCTGCTGGTGAATTACATATTAATTTTTTCTGCTGGTGA
TAAACATTAAATTAATCATGTTTCAAAAAA

FIGURE 147

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45417

<subunit 1 of 1, 500 aa, 1 stop

<MW: 56888, pI: 8.53, NX(S/T): 2

MKCTAREWLRVTTVLFMARAIPAMVVPNATLLEKLLEKYMDDEDGEWWIAKQRGKRAITDNDM
QSILDLHNKLRSQVYPTASNMEYMTWDVELERSAESWAESCLWEHGPA SLLPSIGQNLGAHW
GRYRPPTFHVQSWYDEVKDFSYPYEHECNPYCPFRCSGPVCTHYTQVVWATSNRIGCAINLC
HNMNIWGGIWP KAVYLCNYS PKGNWWGHAPYKHGRPCSACPPSFGGCRENL CYKEGSDRY
YPPREETNEIERQQSQVHDTHVTRSDSSRNEVIS AQQMSQIVSCEVRLRDQCKGTT CNR
YEC PAGCLDSKAKVIGSVHYEMQSSICRAAIHYGIIDNDGGWVDITRQGRKH YFIKSNRNGI
QTIGKYQSANSFTVSKVTQAVTCETTVEQLCPFHKPASHCPRVYCP RNCMQANPHYARVIG
TRVYSDLSSICRAAVHAGVVRNHGGYVDVMPVDKRKTYIASFQNGIFSESLQNPPGGKAPRV
FAVV

Important features:

Signal peptide:

amino acids 1-20

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 protein

amino acids 165-186, 196-218, 134-146, 96-108 and 58-77

N-glycosylation site

amino acids 28-31

FIGURE 148

GCGGAGACAAGCGCAGAGCGCAGCGCACGGCCACAGACAGCCCTGGGCGATCCACCGACGGCG
CAGCCGGAGCCAGCAGAGCCGGAAGGCGCGCCCCGGGCAGAGAAAGCCGAGCAGAGCTGGGT
GGCGTCTCCGGGCGCGGCTCCGACGGGCGAGCGCCCTCCCCATGTCCCTGCTCCCGACGCCG
CGCCCTCCGGTCAGCATGAGGCTCCTGGCGGCGCGCTGCTCCTGCTGCTGTGGCGCTGT
ACACCGCGCGTGTGGACGGGTCCAATGCAAGTGCTCCCGGAAGGGACCCAGATCCGCTAC
AGCGAGCTGAAGAAGCTGGAATGAAGCCAAAGTACCCGCACTGCGAGGAGAAGATGGTTAT
CATCACCACCAAGAGCGTGTCCAGGTACCGAGGTGAGGAGCACTGCCTGCACCCCAAGCTGC
AGAGCACCAAGCGCTTTCATCAAGTGGTACAACGCTTGAACGAGAAGCGCAGGGTCTACGAA
GAATAGGGTGAAAAACCTCAGAAGGGAAAACTCCAACCAGTTGGGAGACTTGTGCAAAGGA
CTTTGCAGATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGCCTTTC
TTTCTCACAGGCATAAGACACAAATTATATATTGTTATGAAGCACTTTTTACCAACGGTCAG
TTTTTACATTTTATAGCTGCGTGCGAAAGGCTTCAGATGGGAGACCCATCTCTCTTGTGCT
CCAGACTTCATCACAGGCTGCTTTTATCAAAAAGGGGAAAACTCATGCCCTTCTCTTTTAA
AAAATGCTTTTTTGTATTTGTCCATACGTCACTATACATCTGAGCTTTATAAGCGCCCGGA
GGAACAATGAGCTTGGTGGACACATTTCAATTGCAGTGTGCTCCATTCTAGCTTGGGAAGC
TTCGCTTAGAGGCTCTGGCGCCTCGGCACAGCTGCCACGGGCTCTCTGGGCTTATGGCCG
GTCACAGCCTCAGTGTGACTCCACAGTGGCCCTGTAGCCGGCAAGCAGGAGCAGGTCTCT
CTGCATCTGTTCTCTGAGGAACCAAGTTTGGTTGCCAGAAAAATGTGCTTCATTCCCCCT
GGTTAATTTTTACACACCCTAGGAAACATTCCAAGATCCTGTGATGGCGAGACAAATGATC
CTTAAAGAAGGTGTGGGCTCTTTCCCAACCTGAGGATTTCTGAAGGTTTACAGGTTCAATA
TTTAATGCTTCAGAAGCATGTGAGGTTCCCAACACTGTGACGCAAAAACCTTAGAGAGAAAACT
TAAAAATATATGAATACATGCGCAATACACAGCTACAGACACACATTTCTGTGACAAGGGAA
AACCTTCAAAGCATGTTTCTTCCCTCACCACAACAGAACATGCAGTACTAAAGCAATATAT
TTGTGATTTCCCATGTAATTCTTCAATGTTAAACAGTGCAGTCTCTTTTCGAAAGCTAAGAT
GACCATGCGCCCTTCTCTGTACATATACCTTTAAGAAGCGCCCCCTCCACACACTGCCCC
CAGTATATGCCGCAATTGTACTGCTGTGTTATATGCTATGTACATGTGAGAAACCATTAGCAT
TGCATGCAAGTTTCATATTCTTTCTAAGATGGAAAGTAATAAAATATATTTGAAATGTAAAA
AAAAAAAAAA

FIGURE 149

MSLLPRRAPPVSMRLAAALLLLLLALYTARVDGSKCKSRKGPKIRYSDVKKLEMKPKYPH
CEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIKWYNWNEKRRVYEE

Signal sequence:

amino acids 1-34

MSLLPRRAPPVSMRLAAALLLLLLALYTARVDGSKCKSRKGPKIRYSDVKKLEMKPKYPH
CEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIKWYNWNEKRRVYEE

FIGURE 150

GCCCCAGGGACTGCTATGGCTTCCTTTGTTGTTACCCCGGTCTGCGTCATGTTAAACTCCAATGTCTCTGTG
 GTTAACTGCTCTTGGCATCAAGTTCACCTCATTTGACAGCCAAGCACAGTATCCAGTTGTCAACACAAATTTATGG
 CAAAATTCGGGGCTTAAGAACCCGTTACCCAAATGAGATCTTGGGTCAGTGAGCAGTACTTGAAGGTCCTCTA
 TGCTTCACTCCGCCCCACTTGGAGAGAGGGCGGTTTTCAGCCCCCAGAACCCCGTCTCTCTGGACTGGCATCGAAATATC
 TACTCAGTTTGTGCTGTGTGTGCCCCAGCACCTGGATGAGAGATCTTACTGTCATGATGCTGCTGCCCCATCTG
 TACCGCCAATTTGGATACTTTTGTAGACTTATGTTCAAGATCAAAATGAAGACTGCTGCCCCATCTGCTG
 CCCCAGGAAGATGGAGCCCAACAAAGAAAACGCGAGATGATATAACAGGTAATGACCGTGGTGAAGACGGAAGA
 TATTCTATGATCAGAACAGTAAGAAGCCCGTCTGTTTATCCATGGGGGATCTTACATGGAGGGCACCGGCAA
 CATGATTGACGGCAGCATTTTGGCAGCTACGCGAAACGTCATCGTATCACCATTAACTACCGTCTGGGAATACT
 AGGGTTTTTAAGTACCGGTGACGAGCAGCAAAAGGCAACTATGGGCTCTGGATCAGATTTCAAGCACTGCGGTG
 GATTGAGAGAAATGTGGGAGCCTTTGGCGGGGACCCCAAGAGAGTGCACATCTTTGGCTCGGGGGCTGGGGCTC
 CTGTGTGTCAGCCTGTTGACCTGTCCCACTACTCAGAAGGTTCTTTCCAGAAGGCCATCATTCAGAGCGGCACCGC
 CTTGTCCAGCTGGGCAGTGAATACCAAGCCGGCCAAAGTACACTCGGATATTGGCAGACAAGGTGCGGTGCAACAT
 GCTGGACACCACGGACATGGTAGAATGCTTGGGAAACAAGAACTACAGGAGCTCATCCAGCAGACCATCACCCC
 GGGCACCTACCCATAGCTTTCGGGCGGTGATCGAGCGGACGTCATCCAGCAGCAACCCAGATCTGTATGGA
 GCAAGGCGAGTTCCTCAACTACGACATCATGCTGGGCTCAACCAAGGGGAAGGCTGAAAGTTGCTGGACGGCAT
 CGTGATAACGAGGACGGTGTGACGCCCAACGACTTTGACTTCTCGTGTCCAACCTTCTGGGACCACTTTACGG
 CTACCTTGAAGGGAAAGACACTTTTGGGGAGACTATCAAGTTCATGTACACAGACTGGGCGGATGAAGAAAACCC
 GGAGACGCGCGGAAAACCTTGGTGGCTCTTTACTGACCAACAGTGGGTGGCCCCCGGCTGGCGCGAGCT
 GCACGCGAGTACGGCTCCGCCACTACTTCTATGCTTCTATCATCACTGCCAAAGGAAATGAAGCCAGCTG
 GGCAGATTGCGGCCATGTGTATGAGGTCCCTATGTCTTGGCATCCCCATGATCGGTCCACOGAGCTCTCAG
 TTGTAACTTTTCCAAGAACGAGCTGATGCTCAGCGCGGTGTCATGACCTACTGGAAGCAATTCGCCAAAATGG
 TGATCCAAATCAACAGTTCCTCAGGATACCAAGTTCATTCACAAAACCCCAACCGCTTTGAAGAGATGGGCTG
 GTCCAAGTATAATCCCAAGACAGCTCTATCTGCATATTGGCTTGAACCCAGAGTGAGAGATCACTACCGGGC
 AACGAAAGTGCTTTCTGGTTGGAATCGTTCCTCATTTGCAACACTTGAACGAGATATCCAGTATGTTTCAAC
 AACCAAAAGGTTCTCCACCAGACATGACATCATTTCCCTATGGCAGCCGCTCCCGCCAGATATGGCC
 AACCAACCAACGCGCCAGTAACTCTCTGCCAACAAATCCCAACACTCTTAAGGACCTTCAACAAACAGGGCCTGA
 GGACACAACCTGCTCTTCACTAGAGTATAGCTTTTGGCGGCTGTACTACAAAAGAGCAAGAGGCGCATGAGATCAGAG
 GCGCCCCAGTCCCCAGAGAAACACCAACAAATGATATCGCTCACATCCAGAACGAAGAGATCATGCTCTGAGAT
 GAAGCAGCTGGAAACAGATCAGGAGTGTGAGTCTGCTGACGSCACACGACACACTGAGGCTCAGCTGCCCGCAG
 CTACACCTCAGCTGCGCGGTGCCAGATGACATCCCACTTATGACGCGCAACACCATCACCATTGATTCACAA
 CACACTGACGGGGGTCAGCGCTTTCACACTTTTAAACCTTTCAGTGGAGGACAAAACAGTACAAATTTACCCCA
 CGGAACTTCAACACTAGAGTATAGCTTTTGGCCCTATTTCCCTTCTCTCTGCTTCCGCTCGGGGCGTC
 AGAAGAGGGGAAGGAAGAGATAAGGAAAGAGAGAGAGAAAGAGTCTCCAGACCAGGAATGTTTTGTGCCACT
 GACTTAAGACAAAATTCGAAATGTGAGAAGTACACTTTCTGTTAAATAAGTCTTAAAGATCTTACCA
 CTCCTCAATCAATGTTAGTGTGATAGGACATCACCATTTCAGGCCCCGGGTGTTTCCAAAGTTCATGGAAGCAGCT
 GACACTTCTGAAACTCAGCCAAGGACACTTGATATTTTAAATTAAGTGAAGTTTAAACTTTCTTCTGTG
 CACACATGATGGCTCTCTTAAAGTGAAGAAAGATCAATGAGATTTTGCCACGACATGGAGCTGTAATCCAG
 AGAGAGGAACGTAGAAATTTTATTAATAAAGAAATGGACTGTGACGCAAAATCTGTACGGTCTGTGCAAGAG
 GTGTTTGGCAGCCTGAACATATATTAAGAGACTTTGT

100706.10404

FIGURE 151

MLNSNVLLWLTALAIAKFTLIDSQAQYFVVNTNYGKIRGLRTPLPNEILGPVEQYLGVVPYASP
PTGERRFQPEPPSSWTGIRNTTQFAAVCFQHLDERSLLHDMPLIWFATANLDTLMTYVQDQN
EDCLYLNIVVPTEDGANTKKNADDITSNDRGEDEDIHDQNSKKPVMVYIHGGSYMEGTGNMI
DGSILASYGNVIVITINYRLGILGFLSTGDQAAKGNYGLLDQIQALRWIEENVGAFGGDPKR
VTIFGSGAGASCVSLLTSLSHYSEGLFQKAI IQSGTALSSWAVNYQPAKYTRILADKVGCNML
DTTDMVECLRNKNYKELIQQTITPATYHIAFGFVIDGDVIPPDDPQILMEQGEFLNYDIMLGV
NQGEGLKFVDGIVDNEDGVTPNDFDFSNSFVDNLYGYPEGKDTLRETIKFMYTDWADKENP
ETRKRKTLVALFTDHWVAPAVAADLHAQYGSPTYFYAFYHHCQSEMKP SWADSAHGDEVPPV
FGIPMIGPTELFSCNFSKNDVMSAVVMYWTNFAKTGDPNQVPQDTKFIHTKPNRFEEVA
WSKYNPKDQLYLHIGLKPRVRDHYRATKVAFWLELVPHLHNLNEIFQYVSTTTKVPPDMTS
FPYGTRRSPAKIWPTTKRPAITPANNPKHSDPHKTGPEDTTVL IETKRDYSTE LSVTTI AVG
ASLLFLNII LAFAALYYKKDKRRRHETHRRPSPQRNTTNDIAHIQNEEIMSLQMKQLEHDECE
SLQAHDTLRLTCPDYYTLTLRRSPDDIPLMTNTITIMIPNTLTGMQPLHTFNTFSGGQNSTN
LPHGHSTTRV

Signal sequence:

amino acids 1-24

Transmembrane domains:

amino acids 189-204, 675-692

FIGURE 152

GGGAAAGATGGCGGGGACTCTGGGACCCCTTGGGTCGTGGCAGCAGTGGCGGCGATGTTTGT
CGGCTCGGGATGGGTCCAGGATGTTACTCCTTCTCTTTTGTGGGGTCTGGGCAGGGGCCA
CAGCAAGTCGGGGCGGGTCAAACGTTTCGAGTACTTGAACCGGGAGCAGTCTCGTGTGGAAGCC
CTACCAGGGTGTGGGCACAGGCAGTTCTCTCACTGTGGAATCTGATGGGCAATGCCATGGTGA
TGACCCAGTATATCCCGCTTACCACAGATATGCAAAGTAAACAGGGTGCCTTGTGGAAACGGG
GTGCCATGTTTCTGAGAGACTGGGAGTTGCAGGTGCACCTTCAAATCCATGGACAGGAAA
GAAGAATCTGCATGGGGATGGCTTGGCAATCTGGTACACAAAGGATCGGATGCAGCCAGGGC
CTGTGTTTGGAAACATGGACAATTTGTGGGGCTGGGAGTATTGTAGACACCTACCCCAAT
GAGGAGAAGCAGCAAGAGCGGGTATTCCCTACATCTCAGCCATGGTGAACACGGCTCCCT
CAGCTATGATCATGAGCGGGATGGGCGGGCTACAGAGCTGGGAGGCTGCACAGCCATTGTCC
GCAATCTTCATTACGACACCTTCTCGGTGATTCTCGTACGTCAAGAGGCATTGACGATAATG
ATGGATATTGATGGCAAGCATGAGTGGAGGGACTGCATTGAAGTGCCCGAGTCCGCTGCC
CCGCGGCTACTACTTCGGCACCTCTCCATCACTGGGGATCTCTCAGATAATCATGATGTCA
TTTCCTTGAAGTTGTTTGAAGTCAGAGTGGAGAGAACCCAGAGAAGAAAAGCTCCATCGA
GATGTGTTCTTGCCCTCAGTGGACAATATGAAGCTGCCTGAGATGACAGCTCCACTGCCGCC
CCTGAGTGGCTGGCCCTCTTCTCATCGTCTTTTCTCCCTGGTGTGTTTCTGTATTTGCCA
TAGTCATTGGTATCATACTCTACAACAAATGGCAGGAACAGAGCCGAAAGCGCTTCTACTGA
GCCCTCCTGCTGCCACCACCTTTTGTGACTGTCAACCATGAGGTATGGAAGGAGCAGGCAGTG
GCCTGAGCATGCAGCCTGGAGAGTGTCTTGTCTCTAGCAGCTGGTTGGGGACTATATTCTG
TCACTGGAGTTTGAATGCAGGGACCCCGCATTCCTATGGTTGTGCATGGGGACATCTAACT
CTGGTCTGGGAAGCCACCCACCCAGGGCAATGCTGCTGTGATGTGCCTTTCCCTCAGTCC
TTCATGTGGGAGCAGAGGTGTGAAGAGAAATTACGTGGTTGTGATGCCAAATACAGAAC
AGAATTTCATAGCCAGGCTGCCGTGTGTTTGAAGTCTCAGAAGGCCCTTCTACTTCAGTTTGA
AATCCACAAAGAAATAAAACTGGTAACACCAAGGCTTCTGACCATCCATTCTGTGGGTT
TTGCATTTGACCCAAACCCTCTGCCTACCTGAGGAGCTTCTTTGGAAACAGGATGGAACT
TCTTCCCTGCCTTACCTTCCCTTCACTCCATTCAATTGCTCTCTGTGTGCAACCTGAGCTG
GGAAAGGCATTGGATGCCTCTCTGTGGGGCCTGGGGCTGCAGAACACACTGCGTTTCAC
TGGCCTTCATTAGGTGGCCTAGGGAGATGGCTTCTGCTTTGGATCACTGTTCCTTAGCAT
GGGTCTTGGGTCTATTGGCATGTCCATGGCCTTCCAATCAAGTCTCTTCAGGCCCTCAGTG
AAGTTTGGCTAAAGGTTGGTGTAATAATCAAGAGAAGCCTGGAAGACATCATGGATGCCATG
GATTAGCTGTGCAACTGACCAGCTCCAGGTTGATCAAACCAAAGCAACATTTGTGATGTG
GTCTGACCATGTGGAGATGTTTCTGAGACTGTCTAGAGCCTGCTTAGCTGCATGTTTTGTAGT
TACGATTTTGGAAATCCCACTTTGAGTGCTGAAAGTGAAGGAAGCTTCTTCTTACACCTT
GGGCTTGGATATTGCCAGAGAAGAAATTTGGCTTTTCTTCTTAATGGACAAGAGACAGT
TGCTGTCTCATGTTTCCAGTCTGAGAGCAACAGACCCCTCATCATCTGTGCTGGAAGAGTT
CACTGTCAATTGAGCAGCACAGCCTGAGTGCTGGCCTCTGTCAACCTTATTCCACTGCCTTA
TTTGACAAGGGGTTACATGCTGTCTACCTTACTGCCCTGGGATTAATCAGTTACAGGCCAG
AGTCTCCTTGGAGGGCTGGAAGTCTGAGTCTCTTATGAACCTCTGTAGCCTAAATGAAAT
TCTTAAATCAGCGATGGAAACCAAAAAAAAAAAAAAAAAAGGGCGCGACTCTAGAGTCG
ACCTGCAGTAGGATAACAGGGTAATAAGCTTGGCCGCATGG

FIGURE 153

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50911

><subunit 1 of 1, 348 aa, 1 stop

><MW: 39711, pI: 8.70, NX(S/T): 1

MAATLGPLGSWQQWRRCLSARDGSRMLLLLLLLGSGQGPPQVGAGQTFEYLKREHSLSKPYQ
GVGTGSSSLWNLGMNAMVMTQYIRLTPDMQSKQCALWNRVPCFLRDWELQVHFKIHGQGKKN
LHGDGLAIWYTKDRMQPGPVFGNMDKFVGLGVFVDTPNEEKQQQERVFFYISAMVNNGSLSY
DHERDGRPTELGGCTAIVRNLHYDTFLVIRYVKRHLTIMMDIDGKHEWRDCIEVPGVRLPRG
YYFGTSSITGDLSDNHDVISLKLPELTVERTPEEEKLHRDVFLPSVDNMKLPENTAPLPPLS
GLALFLIVFFSLVFSVFAIVIGIILYNKWQEQSRKRFY

Signal sequence:

amino acids 1-38

Transmembrane domain:

amino acids 310-329

FIGURE 154

CCGAGCCGGGGCGCGCAGCGACGGAGCTGGGGCCGGCCTGGGACCATGGGCGTGAGTGCAATCTACGGATCAGTCT
 CTGATGGTGGGTCGTAACTCAGTGGGGACTCCAAGATTTCATGAAGAAATCAGTTGTCTTCATTCAAGAAT
 TGGGGTCTGGCTCAGAATTCCTGCAGCTGTGTGAAATCTGTTTCTAGAAGAGGTTAATTAATGCTCGAGTCT
 GACATGTTCCCGATTGAGGTGAAACCATGAAGAGAAATAGAATACTTTAATAATGCTTTTTCCGCAACCGCTTCT
 TGCTGTGCTGGCCCTGGCTGCGCTCTGGCCCTTTGTGAGCCTCAGCCTCGAGTCTTCCACCTGATCCCGGTGT
 CGACTCCTAAGAATGGAATGAGTACGAAGAGTCCGAAGAGAAATCATGCCGAGCCCTGTGACGGAGCCCTGTGA
 CAGACCCGCTTTTAAGACTCTTTTGTACTGCAACATCCCAAGTGTGGCGAGCGCAGCATGGAAGGTATGCC
 CGCATCCTTTAAAGCTGTCTCAGTGCATGTGTTCAITCGCAACGGAGAGGTACCACTGTATGTCATTCCCA
 AAACAAGCGACCCAGAAATTTGATGCACTCTGCTGGCTTAACAGGAAACCGTATCACCCAAAACCTGGAAGCTTCA
 TTGATCACAATGTCAAAGAGTCCGGAGCCTCTTTGAAAGCCCTTGAATCCTTGGCTCTTTACCCAAATCACC
 CATTTGTGAGATGGAGAGCTCACACAGACAGGAGTTGTGCAGCATTGTGAGAAACGGTCAAGTGTGAGGGATA
 TCTATCTAAAGAAACCAAACTCCTGCCAATGATTGGTCTGCAGACCAAGCTCTATTAGAGACCACTGGGAAAA
 GCGGAGCCCTACAAGATGGGCTGGCCTTGCTTTATGGCTTTCTCCAGATTTTGACTGGAAGAAGATTTATTTCA
 GGCACCAAGCAAGTGGCTGTTCTGCTCTGGAAGCTGCTATTGCCCGTAAGAAACAGTATCTGGAAGAGGAGC
 AGCGTCGTCAAGTCTCTCACTGTTGAAACCAAGCTGGAGAGACCTACGGGGAGATGGCCAAAGATCGTGG
 ATGTCCCCACCAAGCAGCTTAGAGCTGCCAACCCCATAGACTCATGCTCTGCCACTTCTGCCACAATGTCAGCT
 TTCCTCTGACCAAGAAATGGCTGTGTGACATGGAGCACTCAAGGTAAATTAAGACCATCAGATCGAGGATGAAA
 GGGAAAGACGGGAGAAGAAATTTGACTTCGGGTATTCTCTCTGGGTGCCACCCCATCTGAAACCAACCATCG
 GCGGATGTCAGCGTGGCCACCGAGGGCAGGAAAGAGAGCTTTGCCCTCTACTCTGCTCATGATGTCACTCTGT
 CACCAAGTTCAGTGCTTTGGGCTTTGAGAGCCAGGTTCCCAAGGTTTGCAGCCAGGTTGATCTTTGAGCTTT
 GGCAGACAGAGAAAGCCAGTGAACATTCGCTCGGATTTCTTACAATGGCGTGCATGTCACTTTCCACACT
 CTTTCTGCCAAGACCAACAAGCGTTCTCCCAAGCCATGTGCCGCTTGAAACCTTGGTCCGCTTTGTGAARA
 GGGACATGTTTGTAGCCCTGGGTGGCAGTGGTACAATATTATGATGATGTGCAGGGAGAGATTCTAAAGG
 TATGCACTACAGCAGTATAGAATCCATGCCAATACAGAGCATAGGGAAGGTCACTTATGTTTGTCTGTATC
 TAAGGTTAGAAGATTATGCTTTTAAAGGCTAAATATTGTTTGTGGGAACCAAGAGTGGTGGGTTGAACAGT
 AAGCATTGCTGCAATGTGGTACGTGAATGCTTGGTACAATAATGGCCAGTTCAGAGCAATAGAAAGGTACTT
 TATCATAGCCAGACTTCGCTAGAAATGCCAAGTAATATAGTTCAAGACCTGAAGTTGCCAATCCAGATTTGCAC
 TCTTCTGCGCTGCCCATGTTATCTATGTATGGAACCAAGCACTCAACCAAAATTTTTTAACTCTAGACATT
 TTTACTTTGTCCTGTGTAAGATTTCTTGAATGATTATCTAAATAAAGGTTGGCAAACTTTTCTGTAAAGG
 GCCAGATTGTAATAATTTTCAACTAGAACCAAAAGGCCACATACAGTCTCTGTACATACTACTCAACTCTGT
 TTTCTGAAGCAGGAAGGCCACCAAGACAGTACATAAAGGAATATGTGTAGCTGGGTTCCAGGCGACAGAAAA
 GATGGTGAACAGCTTGGCCCTGGGCTGTGTTTGTGACCCCTCATCTAAAAAATAGGCTATACATAAATGTC
 ACTTCCAGCATTTTGAAGACAGGTTGAATACCAAGAACTTTGAGGTTAAATAAATATGAATAGAATGAATCA
 AACTGATTAGAAGAACTACTTGAAGTTTATGATGATTGTGATACAGATAGTTTAAAGTATGTTCTAAATATTGT
 CTGCTGATCTATTGCTGTATATGCTGAAATTTTGTATGCCATTAGTATTTTATAGTTTAGGAAAAATATT
 TTTCAAGACAGTATTTAGAGTACTTATTCTCTGATGTAATTTCAATTTGCTGACCTGCTGGTGGTTAGAA
 GAGCTAGAAGATGAATCAGGCACTTTCTTCCAATAAACTAATATGGCTCATTCCTTTGACAAGCTGTAGA
 ACTGAGTTCATTTTTAAACCATTTTTCATCAGTTTCAAATGGTAAATTTCAATTTTAAATGCTTTTGGGA
 AGAAGTTTGTCTATTAGGTAGTTTACAGATCTTTATAAGGTGTTTATATATAGAAGCAATTAATATACATCTG
 TGATTTGAACTAATGGTCTAATTTAGAGAAATGGAAGAGTGAAGTGAAGTTCTGTGTGTCATCGGCATTCC
 AACTTTTTCTCTTTGTTTTGTCCAGTGTTCATTGAAATGCTGTTCTATAAAATAAATTTTTTAAGAAATA

CCGAGCCGGGGCGCGCAGCGACGGAGCTGGGGCCGGCCTGGGACCATGGGCGTGAGTGCAATCTACGGATCAGTCT

FIGURE 155

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48329

><subunit 1 of 1, 480 aa, 1 stop

><MW: 55240, pI: 9.30, NX(S/T): 2

MLFRNRFLLLLALALLAFVSLSLQFFHLIPVSTPKNGMSSKSRKRIMPDVTEPPVTDVPY
EALLYCNIPPSVAERSMEGHAPHHFKLVSVHVFI RHGDRYPLYVIPKTKRPEIDCTLVANRKP
YHPKLEAFISHMSKSGSGASFESPLNSLPLYPNHPLCEMGELTQTGVVQHLQNGQLLRDIYLK
KHKL LPNDWSADQLYLETTGKSRTLQSGLALLYGFLPDFDWKKIYFRHQPSALFCSGSCYCP
VRNQYLEKEQRRQYLLRLKNSQLEKTYGEMAKIVDVPTKQLRAANPIDSM LCHFCHNVSFPC
TRNGCVDMEHFKVIKTHQIEDERERREKKLYFGYSL LGAHPILNQTIGRMQRATEGRKEELF
ALYSAHDVTLSPVLSALGLSEARFPRFAARLIFELWQDREKPSEHSVRILYNGVDVTFHTSF
CQDHHKRSPKPMCPLNLVRFVKRDMFVALGGSGTNYYDACHREGF

Signal sequence:

amino acids 1-18

FIGURE 156

AAAAAAGCTCACAAGTTTCTATTAGAGCGAATACGGTAGATTTCCATCCCTTTTGAAGAACAGTACTGTGGA
 GCTATTTAAGAGATAAAACGAAATATCCTTTCTGGGAGTTCAAGATTGTGCAGTAATTGGTTAGGACTCTGAGC
 GCCGCTGTTCAACAAATCGGGAGAGAAAAGCGGAGATCTCTGCTCGCCTTGACACGGCTCGAAGCAAAAGCAGAT
 AGCTAGGAATGAACCAATCCTCGGGAGTATGTGGAACAACGGAGGAGCTCTGACTTTCCCACTGTGCCATTCTAT
 GGGCGAGGAATGCTCTCGACTTCAGTGGTTAAGGGCAGAATGAAAAATAATTCTGGAGGAAGATAAGATATGAT
 TCTTGGCGAGTCTGACCGGAGCTACAAAGGCGTGTCTCTGGGAATCCTCTGGGAGCTCTGTGGGAGACCGG
 ATGCACCCAGATACGCTATTCAAGTTCCGGAGAGCTGGAGAAAGGCTCTAGGGTGGGCGACATCTCCAGGAGCCT
 GGGCTGGAGGCCCGGAGCTCGCGAGCGCGGAGTCCGCATCATCCCAAGGTTAGGACGCAAGCTTTTGGCCT
 GAATCCCGCAGCGGAGCTTGGTCAAGCGGGCAGGATAGACCGGGAGGAGCTCTGTATGGGGGCCATCAAGTG
 TCAATTAAATCTAGACATTTCTGATGGAGGATAAAGTGAAAAATATATGGAGTAGAAGTAGAAGTAAGGGACATTA
 CGACAATGCGCTTACTTTCTGTAAGAGTGAATTAGAAATAAAATTAGTGAAAAATGCAGCCACTGAGATGCGGTT
 CCTCTACCCACAGCCTGGGATCCGATATCGGGAAGAACTCTCTGCAGAGCTACGAGCTCAGCGCCGAACACTCA
 CTTCTCCCTCATGTTGCAAAATGGAGCGCAGCGGTAGTAAGTACCCCGAATTTGGTGCTGAAACCGCGCCTGGACCG
 CGAAGAAAAGGCTGCTCACCACCTGGTCTTACGCGCTCCGACGGGGCGACCCGGTGGCAGCAGGACCCGGCG
 CATCCGCGTGAATGTTCTGGATGCGAAGACAACGACACCGGCTTTGCTCAGCCGAGTACCAGCGCAGCGTTCC
 GGAGATCTGGCCTTGGGCAACGAGCTGCTTGTAGTCAACGCTACCGACCTGACGAGGAGTCAATCGGGAAGT
 GAGGTATTCCTTCGGTATGTGGACGACAAGCGCGCCAAAGTTTCAAACCTAGATTGTAATTGAGGACAATATC
 AACAAATAGGGGAGTTGGACCAAGGAGTCAGGATTTACAGATGGAAGTGCAAGCAATGGATAATGAGGATA
 TTCTGCGCGAGCCAAAGTCTCTGATCACTGTTCTGAGCTGAACGACAATGCCCAAGAGTGGTCTCACTCTCT
 CGCCAGCTCGGTTCCCGAAAACTCTCCAGAGGGACATTAATTGCCCTTTAAATGTAAATGACCAAGATTCTGA
 GGAAGAACGAGCAGGTGATCTGTTTCAATCCAAAGGAAATCTGCCCTTTAAATAGAAAAATCTTACGGAATTTACTA
 TAGTTTATGACAGACATAGTCTTGGATAGGGAAACAGGTTTCTAGCTTACAACTACAGTGAACCCCACTGACCG
 GGAACCCCGCCCTATCCACGGAATCATATCTGCTGAACGTGGCAGACATCCACGACGAACCCCGCGGTCTT
 CCTCAGGCTCTTATTCCTGTTATATCCAGAGAACAAATCCAGAGGAGTTTCTCTGCTCTGTGACCGCCCA
 CGACCGCTGACTGTGAAGAGAACCGCCAGATCACTTATTCCTGGCTGAGAGAACCACTCCAGAGGCGCAAGCTATC
 GTCTTACGTTGCTCAATCACTCCGACACTGGGCTACTGTATGCGCTGAGCTTCTGACTACGAGGAGTCCGAGA
 CTTGCAAGTGAAGTGAATGGCGGGGACAACGGGCAACCGCCCTCAGCAGCAAGTGTGTTGAGCTTGTCTGT
 CTGGACGAGAACGACAACTCTGTCAGGCGAGCGAGCCGGACTCTCTCGGTGGTGTGACGAGCGGAGTGG
 CACGGCGGAGCCCTGTGAGCAGAGACGCGCTCAAGCAGAGCTCTGATGGCGGTCCAGAGCAACCGGCAAC
 CCTCTCTCCGCACTCTCACTCAGCTGCGGCTGGCCGACAGCATCCCAAGTCTCTGGCGGACTCTGGCAG
 CCTCGAGTCTCCAGCTAACTCTGAAACCTCAGACCTCACTCTGTATCTGGTGGTAGCGGTGGCCCGGTCTCTGT
 CGTCTTCTGGCTTCTGTCTCTCTGCTGCTGCTCAGGCTGGCGGCTGGCAGCAAGTCAAGCTCTCTGCGAGC
 TTTAGGAGCGGCTTGAAGAGCGCGCGCTCGCACTTTGTGGGCTGGAGCGGGTGGCAGGCTTTCTGCGAGAC
 CTATTTCCCAAGGTTTTCCTCACCACGGACTCGCGGAAGAGTCACTGTATCTTCCCCCGGCAATATGACAGA
 CATGCTCTGCGAGCGAGGAGCTTTGAAAAAGCGAGCCCTTTTGTGCTGAGGTGATTCGGATTATTTCTAAAGA
 CAGTCAATGGGTTAATTGAGGTGAGTTTATCAAAATCTTCTTTCTTTTTTTTAAATGCTCTGTCTCCCAAGC
 TGGAGTGGCAGCGGATAGATCATAGCTCACTGCGGCTCAAACTCTAGGCTCAAGCAATATCCCACTTTGCT
 CCGGTGTAAACGGGACTCAGGTGCAAGCCACTACTGTCTGCTATCTATCTATCTATCTATCTATCTATCTAT
 CTATCTATCTATCTATCTATCTTTCTGTACAGCGGAGTCTCACGCTGATCTCCGAGTACTTTGGGAGGC
 CGAGGCGGGTGGATCACTTGAAGTTGGGAGTTTGAGACGAGCTGGAACCAATGGAGAAACCCCGTCTATCTAA
 AAAAAACAAAATAGCCGGGCGTGGTGGTGATGTCTGTAATCCAGCTACTTGGGAGGCTGAGTCAGGAGAAAT
 TGCTTTAACTGGGAGTGGAGGTTGCAATGAGCTGAGATTGTGCCATTGCACTCCAGCTTGGGCAACAGAGTGT
 AAATCTATCTCA

FIGURE 157

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48306

><subunit 1 of 1, 916 aa, 1 stop

><MW: 100204, pI: 4.92, NX(S/T): 4

MIPARLHRDYKGLVLLGILLGTLWETGCTQIRYSVPPEELEKGSRVGDISRDGLGLEPRELAER
GVRIIPRGRTQLFALNPRSGSLVTAGRIDREELCMGAIKQLNLDILMEDKVKIYGVEVEVR
DINDNAPYFRESELEIKISENAATEMRPFLPHAWDPDIGKNSLQSYELSPNTHFSLIVQNGA
DGSKYPELVLRALDREEKAAHHLVLTASDGGDPVRTGTARIRVMVLDDANDNAPAFAPQPEYR
ASVPENLALGTQLLVVNATDPDEGVNAEVRYSFYVDDKAAQVFKLDCNSGTISTIGELDHE
ESGFYQMEVQAMDNAGYSARAKVLTIVLDVNDNAPEVVLTSLASSVPENSPRGTLIALLNVN
DQDSEENGQVICFIQGNLPFKLEKSYGNYSLVTDIVLDREQVPSYNTITVTATDRGTPPLST
ETHISLNVADTNDNPPVFPQASYSAIYIPENNPRGVSLSVTAHDPDCEENAQITYSLAENTI
QGASLSSYVSINSDTGVLYALSSFDYEQFRDLQVKVMARDNGHPPLSSNVSLSLFVLDQNDN
APEILYPALPTDGSTGVELAPRSAEPGYLVTKVVAVDRDSGQNAWLSYRLLKASEPGLFSVG
LHTGEVTRARALLDRDALKQSLVVAVQDHGQPPLSATVTTLTVAVADSIPQVLADLSLESFA
NSETSDLTLYLVVAVAAVSCVFLAFVILLALLRLRRWHKSRLLQASGGGLTGAPASHFVGVD
GVQAFLOTYSHEVSLTDSRKSHLIFPQPNYADMLVSQESFEKSEPLLLSGDSVFSKDSHGL
IEVSLYQIFFLFFNCVSQAGVQRYDHSSLRPQTPRLKQLSHLCLRCNRDRCCKPPTVCLSL
IYLSIYLSIYLSIYLLSCTDGSITPVIPLVWEAEAGGSPEVGSRLRPA

Signal sequence:

amino acids 1-30

Transmembrane domains:

amino acids 693-711, 809-823, 869-888

FIGURE 158

CCCAGGCTCTAGTGCAGGAGGAGAAGGAGGAGGAGCAGGAGGTGGAGATTCCAGTTAAAAG
GCTCCAGAATCGTGTAACAGGCAGAGAACTGAAGTACTGGGGCCTCCTCCACTGGGTCCGAA
TCAGTAGGTGACCCCGCCCCCTGGATTCTGGAAGACCTCACCATGGGACGCCCCGACCTCGT
GCGGCCAAGACGTGGATGTTCTCTGCTCTTGCTGGGGGAGCCTGGGCAGGACACTCCAGGGC
ACAGGAGGACAAGGTGCTGGGGGGTCATGAGTGCCAACCCATTGCGAGCCTTGGCAGGCGG
CCTTGTTCCAGGGCCAGCAACTACTCTGTGGCGGTGTCCTTGTAAGGTGGCAACTGGGTCTT
ACAGCTGCCCACTGTAAAAAACCGAAATACACAGTACGCCTGGGAGACCACAGCCTACAGAA
TAAAGATGGCCCAGAGCAAGAAATACCTGTGGTTCAGTCCATCCCACACCCCTGCTACAACA
GCAGCGATGTGGAGGACCACAACCATGATCTGATGCTTCTTCAACTGCGTGACCAGGCATCC
CTGGGGTCCAAAGTGAAGCCCATCAGCCTGGCAGATCATTGCACCCAGCCTGGCCAGAAGTG
CACCGTCTCAGGCTGGGGCACTGTCACCACTCCCGAGAGAATTTTCTGACACTCTCAACT
GTGCAGAAAGTAAAAATCTTTCCCCAGAAGAAGTGTGAGGATGCTTACCCGGGGCAGATCACA
GATGGCATGGTCTGTGCAGGCAGCAGCAAAGGGGCTGACACGTGCCAGGGCGATTCTGGAGG
CCCCCTGGTGTGTGATGGTGCACTCCAGGGCATCACATCTGGGGCTCAGACCCCTGTGGGA
GGTCCGACAAACCTGGCGTCTATACCAACATCTGCCGCTACCTGGACTGGATCAAGAAGATC
ATAGGCAGCAAGGGCTGATTCTAGGATAAGCACTAGATCTCCCTTAATAAACTCACAACCTCT
CTGGTTC

FIGURE 159

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48336

<subunit 1 of 1, 260 aa, 1 stop

<MW: 28048, pI: 7.87, NX(S/T): 1

MGRPRPRAAKTWMFLLLLGGAWAGHSRAQEDKVLGGHECQPHSQPWQAALFQGQQLLCGGVL
VGGNWWLTAAHCKKPKYTVRLGDHSLQNKDGPEQEI PVVQSI PHPCYNSSDVEDHNDLMLL
QLRDQASLGSKVKPISLADHCTQPGQKCTVSGWGTVTSPRENF PDTLNCAEVKIFPQKKCED
AYPGQITDGMVCAGSSKGADTCQGDSGGPLVCDGALQGITSWGS DPCGRSDKPGVYTNICRY
LDWIKKIIGSKG

Important Features:

Signal peptide:

amino acids 1-23

Transmembrane domain:

amino acids 51-71

N-glycosylation site.

amino acids 110-113

Serine proteases, trypsin family, histidine active site.

amino acids 69-74 and 207-217

Tyrosine kinase phosphorylation site.

amino acids 182-188

Kringle domain proteins motif

amino acids 205-217

[illegible]

AAAA

FIGURE 161

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44184
><subunit 1 of 1, 473 aa, 1 stop
><MW: 50708, pI: 9.28, NX(S/T): 6
MKRASAGGSRLLAWLWLQAWQVAAPCPGACVCYNEPKVTTSCPQQGLQAVPVGIPAAASQRI
FLHGNRISHVPAASFACRNLITLWLHNSVNLARIDAAFTGLALLEQLDLSDNAQLRSVDPA
TFHGLGRLHTLHLDRCGLQELGPGFLFRGLAALQYLYLQDNALQALPDDTFRDLGNLTHLFLH
GNRISSVPERAFRGLHSLDRLLHQNVAHVHPHAFRDLGRLMTLYLFANNLSALPTEALAP
LRLQYLRRLNDNPWVCDRCARPLWAWLQKFRGSSSEVP CSLPQRLAGRD LKRLAANDLQGCA
VATGPYHPIWTGRATDEEPLGLPKCCQPDAAADKASVLEPGRPASAGNALKGRVPPGDSPPGN
GSGPRHINDSPFGTLPGSAEPPLTAVRPEGSEPPGFPTSGPRRRPGCSRKNRTRSHCRLGQA
SGGGGGTGDSESGALPSLTCSLTPLGLALVLWTVLGPC

Important features:

Signal peptide:

amino acids 1-26

Leucine zipper pattern.

amino acids 135-156

Glycosaminoglycan attachment site.

amino acids 436-439

N-glycosylation site.

amino acids 82-85, 179-183, 237-240, 372-375 and 423-426

VWFC domain

amino acids 411-425

FIGURE 162

GGAAAGTCCACGGGGAGCTTGGATGCCAAAGGGAGGACGGCTGGGTCTCTGGAGAGGACTAC
TCACTGGCATATTTCTGAGGTATCTGTAGAATAACACAGCCTCAGATACTGGGGACTTTAC
AGTCCCCACAGAACCGTCTCCAGGAAGCTGAATCCAGCAAGAACAATGGAGGCCACGCGGGA
AGCTCATTTGCAGACAAGGCAAGTCCTTTTTCTCTCTCTCTTTGGGCTTATCTCTGGCG
GGCGCGGCGGAACCTAGAAGCTATCTGTGGTGGAGGAACTGAGGGCAGCTCCTTTGTAC
CAATTTAGCAAAGGACCTGGGTCTGGAGCAGAGGGAATTCTCCAGCGGGGGGTTAGGGTTG
TTTCCAGAGGGAAACAACTACATTTGCAGCTCAATCAGGAGACCGCGATTTTGTTGCTAAAT
GAGAAATGGACCGTGAGGATCTGTGCGGTCAACACAGAGCCTGTGTGCTACGTTTCCAAGT
GTTGCTAGAGAGTCCCTTCGAGTTTTTCAAGCTGAGCTGCAAGTAATAGACATAAACGACC
ACTCTCCAGTATTTCTGGACAAACAAATGTTGGTGAAAGTATCAGAGAGCAGTCCCTCTGGG
ACTACGTTTTCTCTGAAGAATGCCGAAGACTTAGATGTAGGCCAAAACAATATTGAGAACTA
TATAATCAGCCCCAACTCCTATTTTCGGGTCTCACCCGCAACGCGAGTGTAGCCAGGAAT
ACCCAGAGCTGGTGTCTGGACAAAGCGCTGGACCGAGAGGAAGAAGCTGAGCTCAGGTTAACA
CTCACAGCACTGGATGGTGGCTCTCCGCCAGATCTGGCACTGCTCAGGTCTACATCGAAGT
CCTGGATGTCAACGATAATGCCCTGAAATTTGAGCAGCCTTTCTATAGAGTGCAGATCTCTG
AGGACAGTCCGGTAGAGCTTCTGTGTTGTAAGGTCTCTGCCACGGATGTAGACACAGGAGTC
AACGGAGAGATTTCTTACTTTTTCCAAGCTTCAGAAGAGATTGGCAAAACCTTTAAGAT
CAATCCCTTGACAGGAAATTTGAACATAAAAAACAACCTCGATTTTCGAAAAACCTTCAGTCCT
ATGAAGTCAATATTGAGGCCAAGAGATGCTGGAACCTTTTTCTGGAATAATGCACCGTTCTGATT
CAAGTGATAGATGTGAACGACCATGCCCCAGAGTTACCATGTCTGCAATTACAGCCCAAT
ACCTGAGAACCGCCCTGAAACTGTGGTTGCACTTTTCACTGTTTTCAGTGTTCAGATCTTGATTACGGAG
AAAAATGGGAAAAATTAGTTGCTCCATTACAGGAGGATCTACCCCTTCTCTGAAATCCGCGGAA
AACTTTTTACACCTACTAACCGGAGAGACCACTAGACAGAGAAAGCAGAGCGGAATACAACT
CACTATCACTGTCACTGACTTGGGGACCCCTATGCTGATAACACAGCTCAATATGACCGTGC
TGATCGCCGATGTCAATGACAACGCTCCCGCTTACCACCAACCTCTACACCCCTGTTCTGCT
CGCGAGAACACAGCCCGCCCTGCACATCCGACGCTCAGCGTACAGACAGAGACTCAGG
CACCAACGCCAGGTCACCTACTCGCTGCTGCCGCCACAGGACCCGCACTTCCGCTCAGAT
CCCTGGTCTCCATCAACGCGGACAAACGGCCACCTGTTCGCCCTCAGGTTCTTGGACTCAGAG
GCCCTGCAGGGGTTCCAGTTCCGCGTGGCGCTTACAGACCAGGCTCCCCGGCGCTGAGCAG
CGAGGCGCTGCTGCGCGTGGTGGTGTCTGGACGCCAACGACAACCTCGCCCTTCTGCTGTATCC
CGTGCAGAACCGCTCCGCGCCCTGCACCGAGCTGGTGCCCCGGGCGGCGAGCCGGCTAC
CTGGTGACCAAGGTGGTGGCGGTGGACGGCGACTCGGGCCAGAACCGCTGGCTGTGCTACCA
GCTGCTCAAGGCCACGGAGCTCGGTCTGTTCCGCGTGTGGGCGCAATGGCGAGGTGCGCA
CCGCCAGGCTGCTGAGCGAGCGCGACGCGGCCAAGCACAGGCTGGTGGTGTCTGGTCAAGGAC
AATGGCGAGCCTCCGCGCTCGGCCACCGCCACGCTGCACGTGCTCCTGGTGGACCGCTTCTC
CCAGCCCTACCTGCCCTCCCGGAGGGCGGCCGACCCAGGCCACGCGCTTGGCTCAGCG
TCTACCTGGTGGTGGCGTTGGCCCTCGGTGTCTTCTGCTCTTCTTTTCGGTGCTCCTGTTC
GTGGCGGTGCGGCTGTGTAGGAGGAGCAGGGCGGCTCGGTGGGTGCTGCTGTTGTCGCGA
GGGCCCCCTTCCAGGCACTCTGTGGACATGAGCGGCACAGGACCTATCCCAAGCTTACC
AGTATGAGGTGTCTTGGCAGAGGGCTCAGGACCAATGAGTTCAAGTTCTCTGAAGCCGATT
ATCCCCAATCTCCCTCCCGAGTGCCCTGGGAAAGAAATCAAGGAAATCTACCTTCCCCAA
TAACCTTTGGGTCAATATTCACTGAGCCATAGTTGACTTTTACCTTCATAGGTATTTTATT
TGTGGCAATTTCCATGCCAATGTTATTTCGCCCAATTTGTGTGTATGTAATATTGTACGGAT
TTACTCTGATTTTTCTCATGTTCTTCTCCCTTGTTTTTAAAGTGAACATTACCTTTATT
CCTGTTCTTT

FIGURE 163

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48314

<subunit 1 of 1, 798 aa, 1 stop

<MW: 87552, pI: 4.84, NX(S/T): 5

MEASGKLICRQRQVLFSLFLGLSLAGAAEPRSYSVVEETEGSSFVTNLAKDLGLEQREFSR
RGVRVVSRGNKHLHLQLNQETADLLNEKLDREDLCGHTEPCVLRQVLLSPFEFFQAEQV
IDINDHSPVFLDKQMLVKVSESSPPGTTFFPLKNAEDLDVGQNNIENYIISPNSYFRVLTRKR
SDGRKYPELVLDKALDREEEAELRLTLTALDGGSPPRSGTAQVYIEVLDVNDNAPEFEQPFY
RVQISEDSPVGFLVVKVSATDVDTGNGEISYSLFQASEEIGKTFKINPLTGEIELKKQLDF
EKLQSYEVNIEARDAGTFSGKCTVLIQVIDVNDHAPEVTMSAFTSPIPENAPETVVALFSVS
DLDSGENGKISCISIQEDLPFLLKSAENFYTLTTERPLDRESRAEYNITITVTDLGTPLMITQ
LNMTVLIADVNDNAPAFQTQTSYTLFVRENNSPALHIRSVSATDRDSGTNAQVTYSLPPQDP
HLPLTSLVSINADNGHLFALRSLDYEALQGQFRVGASDHGSPALSSEALVRVVVLDANDNS
PFVLYPLQNGSAPCTELVPRAAEPGYLVTKVVAVDGDSGQNAWLSYQLLKATELGLFGVWAH
NGEVRTARLLSERDAAKHRLVVLVKDNGEPPRSATATLHVLLVDGFSQPYLPLPEAAPTQAQ
ADLLTVYLVVALASVSSLFLFSVLLFVAVRLCRRSRAASVGRCLVPEGPLPGHLVDMSGTRT
LSQSYQYEVCLAGSGGTNEFKLPKPIIPNFPQCPGKEIQGNSTFPNNFGFNIQ

Important features:

Signal peptide:

amino acids 1-26

Transmembrane domain:

amino acids 685-712

Cadherins extracellular repeated domain signature.

amino acids 122-132, 231-241, 336-346, 439-449 and 549-559

ATP/GTP-binding site motif A (P-loop).

amino acids 285-292

N-glycosylation site.

amino acids 418-421, 436-439, 567-570 and 786-789

FIGURE 164

ACCCACGCGTCCGCCCCACGCGTCCGCCCCACGCGTCCGCGCGTAGCCGTGC
GCCGATTGCCTCTCGGCCTGGGCAATGGTCCCGGCTGCCGCTCGACGACCGCCCCGCGTCAT
GCGGCTCCTCGGCTGGTGGCAAGTATTGCTGTGGGTGCTGGGACTTCCCGTCCGCGGCGTGG
AGGTTCAGAGGAAAGTGGTCGCTTATGGTCAGAGGAGCAGCCTGCTCACCTCTCTCAGGTG
GGGGCTGTGTACCTGGGTGAGGAGGAGCTCCTGCATGACCCGATGGGCCAGGACAGGGCAGC
AGAAGAGGCCAATGCGGTGCTGGGGCTGGACACCCAAGGCGATCACATGGTGATGCTGTCTG
TGATTCTTGGGGAAGCTGAGGACAAAGTGAGTTCAGAGCCTAGCGGCGTCACCTGTGGTGCT
GGAGGAGCGGAGGACTCAAGGTGCAACGTCGAGAGAGCCTTTTCTCTGGATGGCGCTGG
AGCACACTTCCCTGACAGAGAAGAGGAGTATTACACAGAGCCAGAAGTGGCGGAATCTGACG
CAGCCCCGACAGAGGACTCCAATAACACTGAAAGTCTGAAATCCCCAAAGGTGAACTGTGAG
GAGAGAAACATTACAGGATTAGAAAATTTCACTCTGAAAATTTTAAATATGTCACAGGACCT
TATGGATTTTCTGAACCCAAACGGTAGTGACTGTACTCTAGTCCTGTTTTACACCCCGTGGT
GCCGCTTTTCTGCCAGTTTGGCCCTCACTTTAACTCTCTGCCCCGGGCATTTCCAGCTCTT
CACTTTTGGCACTGGATGCATCTCAGCACAGCAGCCTTTCTACCAGGTTTGGCACCGTAGC
TGTTCCCTAATATTTTATTATTTCAAGGAGCTAAACCAATGGCCAGATTTAATCATACAGATC
GAACACTGGAAACTGAAAATCTTCATTTTAAATCAGACAGGTATAGAAGCCAAGAAGAA
GTGGTGGTAAGTCAAGCCGACCAATAGGCCCTCTTCCAGCACTTTGATAAAAAAGTGTGGA
CTGGTTGCTTGATTTTCTTATTCTTTTAAATAGTTTTATTATGTATGCTACCATTCGAA
CTGAGAGTATTCGGTGGCTAATTCAGGACAAGAGCAGGAACATGTGGAGTAGTGATGGTCT
GAAAGAAGTTGGAAAGAGGAACCTCAATCCTTCGTTTCAGAAATTAGTGCTACAGTTTCATA
CATTTTCTCCAGTGACGTGTTGACTTGAAACTTCAGGCAGATTAAAGAATCATTTGTTGAA
CAACTGAATGTATAAAAAAATTATAAACTGGTGTTTAACTAGTATTGCAATAAGCAAATGC
AAAAATATTCAATAG

FIGURE 165

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48333

><subunit 1 of 1, 360 aa, 1 stop

><MW: 39885, pI: 4.79, NX(S/T): 7

MVPAAGRPRPRMRLLGWWQVLLWVLGLPVRGVEVAEESGRLWSEEQPAHPLQVGAVYLGEE
ELLHDPMGQDRAAEEANAVLGLDTQGDHVMVLSVIPGEAEDKVSSEPSGVTGAGGAEDSRC
NVRESLFSLDGAGAHFPDREEEYYTEPEVAESDAAPTEDSNNTESLKSPPKVNCEERNITGLE
NFTLKILNMSQDLMDFLNPNGSDCTLVLPYTPWCRFSASLAPHFNSLPRAFPALHFLALDAS
QHSSLSTRFGTVAVPNILLFQGAKPMARFNHTDRTLETCLKIFIPNQTGIEAKKNVVVTQADQ
IGPLPSTLIKSVDWLLVFSLFFLISFIMYATIRTESIRWLIPGQEQEHVE

Important features:

Signal peptide:

amino acids 1-25

Transmembrane domain:

amino acids 321-340

Homologous region to dilsufide isomerase

amino acids 212-302

N-glycosylation site.

amino acids 165-168, 181-184, 187-190, 194-197, 206-209, 278-281
and 293-296

Thioredoxin domain

amino acids 211-227

FIGURE 166

CCCGGCTCCGCTCCCTCTGCCCCCTCGGGGTGCGCGCCCCACGATGCTGCAGGGGCCCTGGCT
CGCTGCTGCTGCTCTTCTCTGCGCTCGCACTGCTGCGCTGGGCTCGGCGCGCGGGCTCTTCTCTC
TTTGCCAGCCCCGACTTCTCTACAAGCGCAGCAATTGCAAGCCCATCCCGGTCAACCTGCA
GCTGTGCCACGGCATCGAATACCAGAACATGCGGCTGCCCAACCTGCTGGGCCACGAGACCA
TGAAGGAGGTGCTGGAGCAGGCCGCGCTTGATCCCGCTGGTCATGAAGCAGTGCCACCCG
GACACCAAGAAGTTCTGTGCTCGCTCTTCGCCCCGTGCTGCCTCGATGACCTAGACGAGAC
CATCCAGCCATGCCACTCGCTCTGCGTGCAAGTGAAGGACCGCTGCGCCCCGGTCATGTCCG
CCTTCGGCTTCCCCTGGCCCGACATGCTTGAGTGCGACCGTTTTCCCCCAGGACAACGACCTT
TGCATCCCCCTCGCTAGCAGCGACCACTCTGCCAGCCACCGAGGAAGCTCCAAAGGTATG
TGAAGCCTGCAAAAATAAAAATGATGATGACAACGACATAATGGAAACGCTTTGTAAAAATG
ATTTTGCACTGAAAATAAAAGTGAAGGAGATAACCTACATCAACCGAGATACAAAATCATC
CTGGAGACCAAGAGCAAGACCATTACAAAGCTGAACGGTGTGTCCGAAAGGGACCTGAAGAA
ATCGGTGCTGTGGCTCAAAGACAGCTTGCAAGTGCACCTGTGAGGAGATGAACGACATCAACG
CGCCCTATCTGGTCATGGGACAGAAACAGGGTGGGGAGCTGGTGATCACCTCGGTGAAGCGG
TGGCAGAAGGGGCAGAGAGAGTTCAAGCGCATCTCCCGCAGCATCCGCAAGCTGCAGTGCTA
GTCCCGGCATCCTGATGGCTCCGACAGGCCTGCTCCAGAGCACGGCTGACCATTTCTGTCTC
GGGATCTCAGCTCCCGTTCCCCAAGCACACTCCTAGCTGCTCCAGTCTCAGCTGGGCAGCT
TCCCCTGCCTTTTCACAGTTTGCATCCCCAGCATTTCTGAGTTATAAGGCCACAGGAGTG
GATAGCTGTTTTACCTAAAGGAAAAGCCCACCGAATCTGTAGAAATATTCAAACCTAATA
AAATCATGAATATTTTAA

FIGURE 167

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50920

><subunit 1 of 1, 295 aa, 1 stop

><MW: 33518, pI: 7.74, NX(S/T): 0

MLQGPGSLLLLFLASHCCLGSARGLFLFGQPDFSYKRSNCKPIPVNLQLCHGIEYQNMRLPN
LLGHETMKEVLEQAGAWIPLVMKQCHPDTKKFLCSLFAPVCLDDLDLDETIQPCHSLCVQVKDR
CAPVMSAFGFPWPDMLECDRFPQDNDLCIPLASSDHLLPATEEAPKVCEACKNKNDNDNDIM
ETLCKNDFALKIKVKEITYINRDTKIILETKSKTIYKLNQVSEKDLKKSVLWLKDSLQCTCE
EMNDINAPYLVMGQKQGGLVITSVKRWQKQREFKRISRIRKLQC

Important features:

Signal peptide:

amino acids 1-20

Cysteine rich domain, homologous to frizzled N terminus

amino acids 6-153

FIGURE 168

GTGGAGGCCGCCGACGATGGCGGGGCCGACGGAGGCCGAGACGGGGTTGGCCGAGCCCCGGG
CCCTGTGCGCGCAGCGGGGCCACCGCACTACGCGCGCGCTGGGTGTTCTGCTCGCGATC
AGCCTGCTCAACTGCTCCAACGCCACGCTGTGGCTCAGCTTTGCACCTGTGGCTGACGTCAT
TGCTGAGGACTTGGTCTGTCCATGGAGCAGATCAACTGGCTGTCACTGGTCTACCTCGTGG
TATCCACCCCATTTGGCGTGGCGGCCATCTGGATCCTGGACTCCGTGCGGCTCCGTGCGGCG
ACCATCCTGGGTGCGTGGCTGAACTTTGCCGGGAGTGTGTACGCATGGTGCCTGCATGGT
TGTTGGGACCCAAAACCCATTGCTTCTCCTCATGGGTGGCCAGAGCCTCTGTGCCCTTGCCC
AGAGCCTGGTCATCTTCTCAGCCAAGCTGGCTGCCTTGTGGTTCCAGAGCACCAGCGA
GCCACGCCAACATGCTCGCCACCATGTGCAACCTCTGGGCGTCTTGTGGCCAATGTGCT
GTCCCTGTGCTGGTCAAGAAGGGTGAGGACATTCGGTTAATGCTCGTGTCTATACCATCC
CTGCTGGCGTCTGCTGCTGCTGCCACCATCTGCTGTGGGAGAGTGTGCCCCCACC
CCCTCTGCCGGGGCTGCCAGCTCCACCTCAGAGAAGTTCTTGATGGGCTCAAGCTGCAGCT
CATGTGGAACAAGGCTATGTATCCTGGCTGTGTGCTTGGGGGAATGATCGGATCTCTG
CCAGCTTCTCAGCCCTCCTGGAGCAGATCCTCTGTGCAAGCGGCCACTCCAGTGGGTTTCC
GGCCTCTGTGGCGCTCTTTCATCACGTTTGGGATCCTGGGGGCACTGGCTCTCGGCCCTA
TGTGGACCGACCAAGCACTTCACTGAGGCCACCAAGATTGGCCTGTGCCCTGTTCTCTG
CCTGCGTGCCCTTTGCCCTGGTGTCCAGCTGCAGGGACAGACCTTGCCCTGGCTGCCACC
TGCTCGCTGCTCGGGCTGTTTGGCTTCTCGGTGGGCCCCGTGGCCATGGAGTTGGCGGTGGA
GTGTTCTTCCCCGTGGGGAGGGGGCTGCCACAGGCATGATCTTTGTGCTGGGGCAGGCCG
AGGGAATACTCATCATGCTGGCAATGACGGCACTGACTGTGCAGCTCGGAGCCGTCTTG
TCCACCTGCCAGCAGGGGGAGGATCCACTTGACTGGACAGTGTCTCTGCTGCTGATGGCCG
CCTGTGCACCTTCTTCACTGTCATCCTGGCGGTCTTCTTCCACACCCATACCGGCGCCTGC
AGGCCGAGTCTGGGGAGCCCCCTCCACCCGTAACGCCGTGGGCGCGCAGACTCAGGGCCG
GGTGTGGACCGAGGGGGAGCAGGAAGGGCTGGGGTCTGGGGCCAGCAGCGGACTCCGGA
GTGCACGGCGAGGGGGGCTCGCTAGAGGACCCAGAGGGCCCGGAGCCCCACCCAGCCT
GCCACCGAGGACTCCCGTGCGCAAGGCCCAGCAGCCACCGACGCGCCCTCCCGCCCGGC
AGACTCGCAGGCAGGGTCCAAGCGTCCAGGTTTATTGACCCGCTGGGTCTCACTCCTCCTT
CTCCTCCCCGTGGGTGATCACGTAGCTGAGCGCCTTGTAGTCCAGGTTGCCCGCCACATCGA
TGGAGGCGAACTGGAACATCTGGTCCACCTGCGGGCGGGGGCGAAAGGGCTCCTTGCGGGCT
CCGGGAGCGAATTACAAGCGCGCACCTGAAAA

FIGURE 169

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50988
><subunit 1 of 1, 560 aa, 1 stop
><MW: 58427, pI: 6.86, NX(S/T): 2
MAGPTEAETGLAEPRALCAQRGHRTYARRWVFLLAISLLNCSNATLWLSFAPVADVIAEDLV
LSMEQINWLSVLVYLVVSTPFGVAAIWILDSVGLRAATILGAWLNFAGSVLRMVPCMVVGTON
PFAFLMGGQSLCALAQSLVIFSPAKLAALWFPEHQRATANMMLATMSNPLGVLVANVLSFVLV
KKGEDIPMLGLVYTIPAGVVCLLSTICLWESVPPTPPSAGAASSTSEKFLDGLKLQLMWNKA
YVILAVCLGGMIGISASFSALLEQILCASGHSSGFSGLCGALFITFGILGALALGPYVDRTK
HFTEATKIGLCLFSLACVPFALVSQQLGQTLALAATCSLLGLFGFSVGPVAMELAVECSFPV
GEGATGMI FVLGQAE GILIMLAMTALT VRRSEPSLSTCQQGEDPLDWTV SLLLMAGLCTFF
SCILAVFFHTPYRRLQAESGEPPSTRNAVGGADSGPGVDRGGAGRAGVLGPSTATPECTARG
ASLEDPRGPGSHPACHRATPRAQGAATDAPSRPGRLAGRVQASRFIDPAGSHSSFSSPWVIT

Important features:

Signal peptide:

amino acids 1-44

Transmembrane domains:

amino acids 61-79, 98-112, 126-146, 169-182, 201-215, 248-268,
280-300, 318-337, 341-357, 375-387, 420-441

N-glycosylation site.

amino acids 40-43 and 43-46

Glycosaminoglycan attachment site.

amino acids 468-471

FIGURE 170

GTCCACATCTCTGCTCAACTGGGTCAAGTCCCTCTTAGACCAGCTCTTGTCCATCATTGTGTAAGTGGACCAAC
TAGTCTCCCACTAGGGGGTCTCCCTGGCAATTCTTGATCGGGTTTGGACATCTCAGATCGCTTCCAATGAAGA
TGGCCTTGGCTTGGGGTCTGCTGTTTTCATAATCATCTAATCTAGGACAAGGTTGGCCCGGCACTCTGGGGG
AAGGAGACCGGGGCTGATCAAGCCATCCAGGAACACTTGGAGGACTTGTCCAGCCTTGAAGAAAGCTCTAGTGGTT
TCTGAATCTAGCCCACTTGGCGGTAAAGCATGATGCAACTTCTGCAACTTCTGCTGGGGCTTTGGGGCCAGGTGG
CTACTTATTTCTTTTAGGAGATGTCTCAGGAGTGAACCACTCTCACGTGAATAATCAAGTCTCAGAGGAAGTGCC
ATCTGGTACAGTGAATCCGGGAAGCTTGTCCAGGAATCTGGCCGGAGGAGCGGAGGCAAGCTGGGGCCCGCTT
CCAGGTGTTGAGCTGCCTCAGGCGCTCCCACTTCAAGTGGACTCTGAGGAAGGCTTGTCTCAGCAAGGAGGGG
GCTGGATCGAGAGCACTGTCCGACAGTGGGATCCCTGCTGTTTCTTGTGATGTCTTCCCAAGGCGAGGAGG
GGCTCTGATCCATGTGGAGATCCAGATGCTGACATCAATGACCCAGCCAGCGGTTGCTCCCAAGGCGAGGAG
GCTGGAATCTCTGAGAGCGCTCTCTGCGAACCAGGATCCCTTGGACAGAGCTCTTGACCCGAGACACAGGCC
TAACACCTGACACCTCACTCTGTCTCCAGTGAGCACTTTGCTTGGATGTCAITGGGGCCCTGTAGGAC
CAACATGACGAATCTCATAGTGGTGAAGGAGCTGGACAGGGAATCCATTCAITTTTTGATCTGTTGTTAACTGC
CTATGACAATGGGAACCCCTCAAGTCAAGTACCAGCTTGGTCAAGGTCAAOGCTTGGACTCCAATGACAATAG
CCCTCGCTTGTGAGAGTTCTCATGCGACTGGAATCCAGGAAGATGTGCACTGGTACGCTTCTCATAAATCT
GACCGACAGACCCCTGACCAAGGCCCAATGGGGAGGTGGAGTTCTTCTCTAGTAAGCACTGCCTCCAGAGGT
GCTGACACCTCTCAGTATGATGCAAGACAGGCCAGGTCATTCTGCTGACCCCTTAGACTGAAAAGAACCC
TGCTTCAAGGTTGATGTTTCAGGCAAGGACCTGGGTCCCAATCTATCCAGCCCAATGCAAGTTCTCATCAA
GGTTCTGATGTCATGACAACATCCCAAGCATCCAGTCACTGGGCTCCCGACCACTCACTGGTGTGAGAAGC
TCTTCCCAAGGACAGTTTTTATGCTCTTGTCTAGGAGATGACTTGGATTGAGGACCAATGTTTGTGCTCACTG
CTGGCTGAGCCAGAGCTGGGCCCACTTCAAGTGAAGAACTAATGGCAACACATACATGTTGTCAACCAATGC
CACATCTGGACAGAGAGCACTGGCCCAATAACCTCACTCTGTTAGCCCAAGACCAAGGACTCCAGCCCTTATC
AGCCAAAGAACCTCAGCATTCAGATCAGTGACATCAACGACATGCACCTGTGTTTGAAGAAAGCAGGTATGA
AGTCTTCCACGCGGAAACCACTTACCTCTCTTCACTTATACCATCAAGCTCATGATGAGCATTTGGCATG
TAATGGAAGAGTCTCATACGCACTCAGGACTCCCAAGTTGCTCACTTAGTAGCTATGATCCCAACAGGAGA
GGTCACTGCTCAGAGGTCTAGAACTATGAAGATGAGCGGCTTGTAGTTCCAGGTTGTCAGAGAGTCAAGCGG
GCAACCCATGCTGATCCAGTGTCTCTGTGTGGTCAAGCTCTTGGATGCCAATGATAATGCCCAAGAGTGT
CAGCTGTGCTCAGCGATGGAAGGCCAGCTCTCCGTCTTGTGAAGCTCTCAAGGACCTGCTGCTGTGCTG
CATCGAGACTCCCAATGCTTGGGCCAGCGGGCACTGACACACTCCATGGCCACTCAGACTCCCGGCCATT
CCTTTTGAACAATGTTGGTCAAGAGATGAGACTCGGGGCAATGGAGAGCCCTTACAGACTCCGCAATGG
AAATGAAGCCCACTCTTCACTCCTCAACCTCATACGGGGCAGCTGTTCTCAATGATCAACAATGCCAGAGCT
CATTTGGGAGTGAAGTGGGAGCTGGAGATAGTAGTAGAGGACAGGGAAGCCCCCTTACAGCTCCAGCCCTGTT
GAGGGTCACTGTTGCTCAGAGTGTGGACCACTGAGGAGTCAAGCCGCAAGCCTGGGGCTTGAAGCTTCAATGCTGGC
GCTGACGAGTCACTGCTGCTGCTGTAATGTTGGGCACTTCCGCTGATCTCTGGCTTGTGATCTTCACTTGGC
GACAGAAAGAAAGGACCAACAGGCCCTCACTGTCCGAGGCCAGGTCACCTACCGCCAGCAGCCAGGAGGCC
CAGCAAAACACATTCAGAAGGCAGACATCCCACTGCTGCTCAGGCTCAGGCTCAGGAGCTGAGCTTGTGAAGT
CGGGCAGTCCACCAAGAGTGTGACAGAGGAGCCGATGATGGAAGCTGGGAGCCCTGCTCGAGGCCCTT
CCACTCTACCCCGACCTGTAACGAGCTGCTGTAATCAAGGCAACAGGAGGACACCGGCGGAGAGCCGAGAGT
GCTGCAAGACAGCTCAACCTCTTTTCAACCATCCAGGCGAGGAATGCTCCCGCGAGAGAACCTGAACCTTCC
CGAGCCCCAGCTGCCACAGGCGCACTTCCAGGCTCTGAAGGTTGCAAGGACGCCCCACAGGAGGCTGAGC
TGGACAGCCAGGCGAGTGAAGAGGCCCAACAGAGGCCACAGCCTCTCTGCAAGCCAGGAGCTTCAAGCTCTC
CAATGCAAGTGTCTCTTCAAGAAAGATCAGGCGCCGCTCAGATCTCGGAGAGCTGCTCGGCTGTCTGTGGC
TGCTTCCGCGAGCGGCAACCTGAGGAGCTCACTGTGATTTCTCTCTGTTTCAAGCAATCTCCAGCTGCT
GCTCTTGTGCTCATCGGCCCAATTTCCAGCCCAACCAACCAACAGGAGAAATAGTACTTGGCCAGCAGGAG
CAGCAGGAGTGCATCTCCAGACAGATGGCCCAAGTGCAAGGCTGAGGCGCAGACAGACGAGCAACAGGAGA
AGGGCTTGTGATCTCTGAAGAGGACTCTCTGTGAAGCAACTGTGAGAAGAGAGCTGTCAAGTCTGCTGGACCC
CAGCAGAGTCTGGCCCTGAGCGGCTGAGCGCCCTGACCAGGCTGGATGGAGACTCTCTTGGCCCTCAC
CACCACTACCTGATGACAAATGTATCTTCCCGGATGCTGACGCCAGGAGGCGGAGGACTTCCAGAGCTTGG
CAGGCAAGGAGCTGCTGTGAAACAGCGCTCCAGCATGCCCCGTGAGGAGCGGCTCCGAGGCGCTGCGGCGCT
CTGCTGCGGAGAGCCCTCAGGTTAGACTTGGCCACCACTGCAAGCTCAGGCTGCAAGGTCAGAGGAGCCAGGTG
AAAGACGGGAGCTGAGGCGCAAGAGCAGAGGAGCAGCAGCAGCAGCAGGCTGCTGTAACCTCTCAGACGCT
CTGATCCAGAAACAGGGGCTGAGGATCTGTGACAAAGAGCTGTTTCTAAATCTTGTACTCTACTAGCTAG
CGGCGGCTTGAGAACTTTAGGGTGACTGATGCTACCCCCACAGGAGGCAAGGCTCCGAGCACTAACCTGAC
TGACAAAGCAGCCCTTTGAAGCACTCTGAGTCTTTTGGAGGACAGGAGCGGTTTGGCTGAGATAGTGT
TCTTGGCAAAACATATGTGGAGCACAAGGCTGAGTCTCTGCGCAGACAGATGCCAGGATATCAGAGCAGG
AAAGGTTGGCTTCTTGGGTGAGCAGGAGTCAAGGGCTGTACCTGGGGGTGCGAGAAATGCTCTTGAACCTAT
CAATAAGGAAAGAGCTAAAAAAGAAAAAAGAAAAA

FIGURE 171

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48331
<subunit 1 of 1, 1184 aa, 1 stop
<MW: 129022, pI: 5.20, NX(S/T): 5
MMQLLQLLLGLLPGGYLFLLGDCQEVTTLTVKYQVSEEVPSGTVIGKLSQELGREERRRQA
GAAFQVLQLPQALPIQVDSEEGLLSTGRRLDREQLCRQWDPLVDFVLATGDLALIHVEIQ
VLDINDHQPRFPFKGEQELEISESASLRTRIPLDRALDPDTGPNTLHTYTLSPSEHFALDVIV
GPDETKHAELIVVKELDREIHSFFDLVLTAYDNGNPPKSGTSLVKVNVLDSDNSPFAESS
LALEIQEDAAPGTLTKLTATDPDQGPNGEVEFFLSKHMPPEVLDTFSIDAKTGQVILRRPL
DYEKNPAYEVDVQARDLGNPIPAHCKVLIKVLVDNDNIPSIHVTWASQPSLVSEALPKDSF
IALVMADDLDSGHNGLVHCWLSQELGHFRLKRTNGNTYMLLTNATLDREQWPKYTLTLLAQD
QGLQPLSAKKQLSIIQISDINDNAPVFEKSRYEVSSTRENNLPSLHLITIKAHADLGLINGKVS
YRIQDSPVAHLVAIDSNTEGVTQAQRSLNVEEMAGFEFQVIAEDSGQPMPLASSVSVVVSLLDA
NDNAPEVVQPVLSDGKASLSVLVNASTGHLLVPIETPNGLGPGAGTDTPLATHSSRPFLTT
IVARADSGANGEPLYSIIRNGNEAHLFILNPHTGQLFVNVTNASSLIGSEWELEIVVEDQGS
PPLQTRALLRVMFVTSVDHLRDSARKPGALSMSMLTVICLAVLLGIFGLILALFMSICRTEK
KDNRAYNCREAESTYRQPKRPQKHIIQKADIHLVPVLRGQAGEPCEVQSHKDVDKEAMMEA
GWDPCQLQAPFFHLTPTLTYRTLNRQNGQAPAESREVLQDVTNLLFNHPRQRNASRENLNLEP
QPATGQPRSRPLKVAGSPTRLAGDQGSSEAPQRPASSATLRRQRHLNGKVSPEKESGPRQ
ILRSLVRLSVAAFAERNPVEELTVDSPPVQQISQLLSLLHQGQFQPKPNHRGNKYLAKPGGS
RSAIPDTDGPSARAGGQTDPEQEELDPEDLSVKQLLEEELSSLLDPSTGLALDRLSAPD
PAWMARLSLPLTTNRYRDNVISPDAAATEEPRTFQTFGKAEAPELSPTGTRLASTFVSEMSSL
LEMLLEQRSSMPVEAASEALRRLSVCGRTLSDLATSAASGMKVQGDGPGKGTGTEKSRGSS
SSSRCL

Important features:

Signal peptide:

amino acids 1-13

Transmembrane domain:

amino acids 719-739

N-glycosylation site.

amino acids 415-418, 582-585, 659-662, 662-665 and 857-860

Cadherins extracellular repeated domain signature.

amino acids 123-133, 232-242, 340-350, 448-458 and 553-563

FIGURE 172

CGGACGCGTGGGCGGACGCGTGGGGGAGAGCCGCAGTCCCGGCTGCAGCACCTGGGAGAAGG
CAGACCGTGTGAGGGGGCTGTGGCCCCAGCGTGTGTGGCTCGGGGAGTGGGAAGTGGAG
GCAGGAGCCTTCCTTACACTTCGCCATGAGTTTCCTCATCGACTCCAGCATCATGATTACCT
CCCAGATACTATTTTTTGGATTGGGTGGCTTTTCTTCATGCGCCAATTGTTTAAAGACTAT
GAGATACGTCAGTATGTTGTACAGGTGATCTTCTCCGTGACGTTTGCATTTTCTTGCACTAT
GTTTGAGCTCATCATCTTTGAAATCTTAGGAGTATTGAATAGCAGCTCCCGTTATTTTCACT
GGAAATGAACCTGTGTGTAATTCGTCTGATCCTGTTTTTCATGGTGCCTTTTACATTGGC
TATTTTATGTGAGCAATATCCGACTACTGCATAAAACAACGACTGCTTTTTTCTGTCTCTT
ATGGCTGACCTTTATGTATTTCTTCTGGAACCTAGGAGATCCCTTTCCCATCTCAGCCCCAA
AACATGGGATCTTATCCATAGAACAGCTCATCAGCCGGGTGGTGTGATTGGAGTGACTCTC
ATGGCTCTTCTTCTGGATTGGTGTGTCAACTGCCCATACCTTACATGTCTTACTTCTCT
CAGGAATGTGACTGCACCGGATATTCTAGCCCTGGAACGGCGACTGCTGCAAAACCATGGATA
TGATCATAAGCAAAAAGAAAAGGATGGCAATGGCAGGAGAACAATGTTCCAGAAGGGGGAA
GTGCATAACAACCATCAGTTTTCTGGGGAATGATAAAAAGTGTTACCACTTCAGCATCAGG
AAGTGAAAATCTTACTCTTATTCAACAGGAAGTGGATGCTTTGGAAGAATTAAAGCAGGCAGC
TTTTCTGGAACAGCTGATCTATATGCTACCAAGGAGAGAATAGAATACTCCAAAACCTTC
AAGGGAAATATTTTAAATTTTCTGGTTACTTTTTCTCTATTTACTGTGTTTGGAAAAATTT
CATGGCTACCATCAATATTGTTTTTGATCGAGTTGGGAAAAAGGATCCTGTCAAGAGGCA
TTGAGATCACTGTGAATTATCTGGGAATCCAATTTGATGTGAAGTTTGGTCCCAACACATT
TCCTTCATTCTTGTGGAATAATCATCGTCACATCCATCAGAGGATTGCTGATCACTCTTAC
CAAGTTCTTTTATGCCATCTCTAGCAGTAAGTCCTCCAATGTGCTATTGCTCTATTAGCAC
AGATAATGGGCATGTACTTTGTCTCCTCTGTGCTGCTGATCCGAATGAGTATGCCTTTAGAA
TACCGCACCATAATCACTGAAGTCCTTGGAGAAGTGCAGTTCAACTTCTATCACCGTTGGTT
TGATGTGATCTTCTGGTCAGCGCTCTCTCTAGCATACTTCTCTATTTGGCTCACAAC
AGGCACCAGAGAAGCAATGGCACCTTGAACTTAAGCCTACTACAGACTGTTAGAGGCCAGT
GGTTTCAAAATTTAGATATAAGAGGGGGGAAAAATGGAACAGGGCCTGACATTTTATAAAC
AAACAAAATGCTATGGTAGCATTTTTTACCCTTCATAGCATACTCCTTCCCCGTGAGGTGATA
CTATGACCATGAGTAGCATCAGCCAGAACATGAGAGGGAGAACTAACTCAAGACAATACTCA
GCAGAGAGCATCCCGTGTGGATATGAGGCTGGTGTAGAGGCGGAGAGGAGCAAGAAACTAA
AGGTGAAAAATACACTGGAACCTCTGGGGCAAGACATGTCTATGGTAGCTGAGCCAAACCGT
AGGATTTCCGTTTTTAAAGTTACATGGAAAAGGTTATAGCTTTGCCTTGAGATTGACTCATT
AAAATCAGAGACTGTAACAAAAAAGGGCGGCCGACTCTAGAGTCG
ACCTGCAGAAGCTTGGCCGCCATGGCCCACTTGTTTATTGCAGCTTATAATG

FIGURE 173

MSFLIDSSIMITSQILFFGFGWLFFMRQLFKDYEIRQYVVQVIFSVTFAFSCTMFELIIFEI
LGVLNSSSRYFHWKMNL CVILLILVFMVPFYIGYFIVSNIRLLHKQRLLFSCLLWLTfMYFF
WKLGDPPILSPKHGILSIEQLISRVGVIGVTL MALLSGFGAVNCPYTYMSYFLRNVTDTDI
LALERRLLQTMDMIISKKKRMAMARRTMFQKGEVHNKPSGFWGMIKSVTTSAGSENLT LIQ
QEVDALEBELSRQLFLETADLYATKERIEYSKTFKGKYFNF LGYFFSIYCVWKIFMATINIVF
DRVGKTDPVTRGIEITVNYLGIQFDVKFWSQHISFILVGI IIVTSIRGLLITLTkFFYAISS
SKSSNVIVLLLAQIMGMYFVSSVLLIRMSMPLEYRTIITEVLGELQFNFYHRWFDVIFLVSA
LSSILFLYL AHKQAPEKQMAP

Important features:

Signal peptide:

amino acids 1-23

Potential transmembrane domains:

amino acids 37-55, 81-102, 150-168, 288-311, 338-356, 375-398,
425-444

N-glycosylation sites.

amino acids 67-70, 180-183 and 243-246

Eukaryotic cobalamin-binding proteins

amino acids 151-160

FIGURE 174

CATGGGAAGTGGAGCCGGAGCCTTCCTTACACTCGCCATGAGTTTCCTCATCGACTCCAGCA
TCATGATTACCTCCCGANACTATTTTTTGGATTGGGTGGCTTTTCTTCNGCGCCAATGTT
TAAAGACTATGAGATACGTCAGTATGTTGTACNGGTGATCTTCTCCGTGACGTTGCCATTT
CTTGACCATGTTTGAGCTCATCATCTTTGAAATCTTNGGAGTATTGAATAGCAGCTCCCGT
TATTTTCACTGGAAAATGAACCTGTGTGTAATTCTGCTGATCCTGGTTNTCATGGTGCCTTT
TTACATTGGCTATTTTATTGTGAGCAATATCCGACTACTGCATAAACAACGACTGCTTTTTT
CCTGTCTCTTATGGCTGACCTTTATGTATTTCAG

12345678910111213141516171819202122232425262728293031323334353637383940414243444546474849505152535455565758596061626364656667686970717273747576777879808182838485868788899091929394959697989910010110210310410510610710810911011111211311411511611711811912012112212312412512612712812913013113213313413513613713813914014114214314414514614714814915015115215315415515615715815916016116216316416516616716816917017117217317417517617717817918018118218318418518618718818919019119219319419519619719819920020120220320420520620720820921021121221321421521621721821922022122222322422522622722822923023123223323423523623723823924024124224324424524624724824925025125225325425525625725825926026126226326426526626726826927027127227327427527627727827928028128228328428528628728828929029129229329429529629729829930030130230330430530630730830931031131231331431531631731831932032132232332432532632732832933033133233333433533633733833934034134234334434534634734834935035135235335435535635735835936036136236336436536636736836937037137237337437537637737837938038138238338438538638738838939039139239339439539639739839940040140240340440540640740840941041141241341441541641741841942042142242342442542642742842943043143243343443543643743843944044144244344444544644744844945045145245345445545645745845946046146246346446546646746846947047147247347447547647747847948048148248348448548648748848949049149249349449549649749849950050150250350450550650750850951051151251351451551651751851952052152252352452552652752852953053153253353453553653753853954054154254354454554654754854955055155255355455555655755855956056156256356456556656756856957057157257357457557657757857958058158258358458558658758858959059159259359459559659759859960060160260360460560660760860961061161261361461561661761861962062162262362462562662762862963063163263363463563663763863964064164264364464564664764864965065165265365465565665765865966066166266366466566666766866967067167267367467567667767867968068168268368468568668768868969069169269369469569669769869970070170270370470570670770870971071171271371471571671771871972072172272372472572672772872973073173273373473573673773873974074174274374474574674774874975075175275375475575675775875976076176276376476576676776876977077177277377477577677777877978078178278378478578678778878979079179279379479579679779879980080180280380480580680780880981081181281381481581681781881982082182282382482582682782882983083183283383483583683783883984084184284384484584684784884985085185285385485585685785885986086186286386486586686786886987087187287387487587687787887988088188288388488588688788888989089189289389489589689789889990090190290390490590690790890991091191291391491591691791891992092192292392492592692792892993093193293393493593693793893994094194294394494594694794894995095195295395495595695795895996096196296396496596696796896997097197297397497597697797897998098198298398498598698798898999099199299399499599699799899910001001100210031004100510061007100810091010101110121013101410151016101710181019102010211022102310241025102610271028102910301031103210331034103510361037103810391040104110421043104410451046104710481049105010511052105310541055105610571058105910601061106210631064106510661067106810691070107110721073107410751076107710781079108010811082108310841085108610871088108910901091109210931094109510961097109810991100110111021103110411051106110711081109111011111112111311141115111611171118111911201121112211231124112511261127112811291130113111321133113411351136113711381139114011411142114311441145114611471148114911501151115211531154115511561157115811591160116111621163116411651166116711681169117011711172117311741175117611771178117911801181118211831184118511861187118811891190119111921193119411951196119711981199120012011202120312041205120612071208120912101211121212131214121512161217121812191220122112221223122412251226122712281229123012311232123312341235123612371238123912401241124212431244124512461247124812491250125112521253125412551256125712581259126012611262126312641265126612671268126912701271127212731274127512761277127812791280128112821283128412851286128712881289129012911292129312941295129612971298129913001301130213031304130513061307130813091310131113121313131413151316131713181319132013211322132313241325132613271328132913301331133213331334133513361337133813391340134113421343134413451346134713481349135013511352135313541355135613571358135913601361136213631364136513661367136813691370137113721373137413751376137713781379138013811382138313841385138613871388138913901391139213931394139513961397139813991400140114021403140414051406140714081409141014111412141314141415141614171418141914201421142214231424142514261427142814291430143114321433143414351436143714381439144014411442144314441445144614471448144914501451145214531454145514561457145814591460146114621463146414651466146714681469147014711472147314741475147614771478147914801481148214831484148514861487148814891490149114921493149414951496149714981499150015011502150315041505150615071508150915101511151215131514151515161517151815191520152115221523152415251526152715281529153015311532153315341535153615371538153915401541154215431544154515461547154815491550155115521553155415551556155715581559156015611562156315641565156615671568156915701571157215731574157515761577157815791580158115821583158415851586158715881589159015911592159315941595159615971598159916001601160216031604160516061607160816091610161116121613161416151616161716181619162016211622162316241625162616271628162916301631163216331634163516361637163816391640164116421643164416451646164716481649165016511652165316541655165616571658165916601661166216631664166516661667166816691670167116721673167416751676167716781679168016811682168316841685168616871688168916901691169216931694169516961697169816991700170117021703170417051706170717081709171017111712171317141715171617171718171917201721172217231724172517261727172817291730173117321733173417351736173717381739174017411742174317441745174617471748174917501751175217531754175517561757175817591760176117621763176417651766176717681769177017711772177317741775177617771778177917801781178217831784178517861787178817891790179117921793179417951796179717981799180018011802180318041805180618071808180918101811181218131814181518161817181818191820182118221823182418251826182718281829183018311832183318341835183618371838183918401841184218431844184518461847184818491850185118521853185418551856185718581859186018611862186318641865186618671868186918701871187218731874187518761877187818791880188118821883188418851886188718881889189018911892189318941895189618971898189919001901190219031904190519061907190819091910191119121913191419151916191719181919192019211922192319241925192619271928192919301931193219331934193519361937193819391940194119421943194419451946194719481949195019511952195319541955195619571958195919601961196219631964196519661967196819691970197119721973197419751976197719781979198019811982198319841985198619871988198919901991199219931994199519961997199819992000200120022003200420052006200720082009201020112012201320142015201620172018201920202021202220232024202520262027202820292030203120322033203420352036203720382039204020412042204320442045204620472048204920502051205220532054205520562057205820592060206120622063206420652066206720682069207020712072207320742075207620772078207920802081208220832084208520862087208820892090209120922093209420952096209720982099210021012102210321042105210621072108210921102111211221132114211521162117211821192120212121222123212421252126212721282129213021312132213321342135213621372138213921402141214221432144214521462147214821492150215121522153215421552156215721582159216021612162216321642165216621672168216921702171217221732174217521762177217821792180218121822183218421852186218721882189219021912192219321942195219621972198219922002201220222032204220522062207220822092210221122122213221422152216221722182219222022212222222322242225222622272228222922302231223222332234223522362237223822392240224122422243224422452246224722482249225022512252225322542255225622572258225922602261226222632264226522662267226822692270227122722273227422752276227722782279228022812282228322842285228622872288228922902291229222932294229522962297229822992300230123022303230423052306230723082309231023112312231323142315231623172318231923202321232223232324232523262327232823292330233123322333233423352336233723382339234023412342234323442345234623472348234923502351235223532354235523562357235823592360236123622363236423652366236723682369237023712372237323742375237623772378237923802381238223832384238523862387238823892390239123922393239423952396239723982399240024012402240324042405240624072408240924102411241224132414241524162417241824192420242124222423242424252426242724282429243024312432243324342435243624372438243924402441244224432444244524462447244824492450245124522453245424552456245724582459246024612462246324642465246624672468246924702471247224732474247524762477247824792480248124822483248424852486248724882489249024912492249324942495249624972498249925002501250225032504250525062507250825092510251125122513251425152516251725182519252025212522252325242525252625272528252925302531253225332534253525362537253825392540254125422543254425452546254725482549255025512552255325542555255625572558255925602561256225632564256525662567256825692570257125722573257425752576257725782579258025812582258325842585258625872588258925902591259225932594259525962597259825992600260126022603260426052606260726082609261026112612261326142615261626172618261926202621262226232624262526262627262826292630263126322633263426352636263726382639264026412642264326442645264626472648264926502651265226532654265526562657265826592660266126622663266426652666266726682669267026712672267326742675267626772678267926802681268226832684268526862687268826892690269126922693269426952696269726982699270027012702270327042705270627072708270927102711271227132714271527162717271827192720272127222723272427252726272727282729273027312732273327342735273627372738273927402741274227432744274527462747274827492750275127522753275427552756275727582759276027612762276327642765276627672768276927702771277227732774277527762777277827792780278127822783278427852786278727882789279027912792279327942795279627972798279928002801280228032804280528062807280828092810281128122813281428152816281728182819282028212822282328242825282628272828282928302831283228332834283528362837283828392840284128422843284428452846284728482849285028512852285328542855285628572858285928602861286228632864286528662867286828692870287128722873287428752876287728782879288028812882288328842885288628872888288928902891289228932894289528962897289828992900290129022903290429052906290729082909291029112912291329142915291629172918291929202921292229232924292529262927292829292930293129322933293429352936293729382939294029412942294329442945294629472948294929502951295229532954295529562957295829592960296129622963296429652966296729682969297029712972297329742975297629772978297929802981298229832984298529862987298829892990299129922993299429952996299729982999300030013002300330043005300630073008300930103011301230133014301530163017301830193020302130223023302430253026302730283029303030313032303330343035303630373038303930403041304230433044304530463047304830493050305130523053305430553056305730583059306030613062306330643065306630673068306930703071307230733074307530763077307830793080308130823083308430853086308730883089309030913092309330943095309630973098309931003101310231033104310531063107310831093110311131123113311431153116311731183119312031213122312331243125312631273128312931303131313231333134313531363137313831393140314131423143314431453146314731483149315031513152315331543155315631573158315931603161316231633164316531663167316831693170317131723173317431753176317731783179318031813182318331843185318631873188318931903191319231933194319531963197319831993200320132023203320432053206320732083209321032113212321332143215321632173218321932203221322232233223432253226322732283229323032313232323332343235323632373238323932403241324232433244324532463247324832493250325132523253325432553256325732583259326032613262326332643265326632673268326932703271327232733274327532763277327832793280328132823283328432853286328732883289329032913292

FIGURE 175

GTGTTGCCCTTGGGGAGGGGAAGGGGAGCCNGGCCCTTTCCTAAAATTTGGCCAAGGGTTTC
TTTNTTGAATTCCGGGTNNGNATACCTTCCCAGAAAATATTTTTTGGATTTGGGGTAGNTT
TTTTTCATGCGCCAATTGTTTAAAGACTATGAGATACGTACGTATGTTGTACAGGTGATNTT
NTCCGTGACGTTTGCATTTTCTTGACCATGTTTGAGCTCATCATNTTTGAAATNTTAGGAG
TATTGAATAGCAGCTCCCGTTATTTTCACTGGAAAATGAACCTGTGTGTAATTCTGCTGATC
CTGGTTTTTCATGGTGCCTTTTTACATTGGCTATTTTATTGTGAGCAATATCCGACTACTGCA
TAAACAACGACTGCTTTTTTCTGTCTNTTATGGCTGACCTTTATGTATTTNTTNTGGAAAN
TAGGAGATCCCTTCCCATTC

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FIGURE 176

CTCGCGCAGGGATCGTCCCATGCCGGGGCTCGGAGCGCGACCCTTGGGGGGGCTCCGGGATTGTGACTTTT
 TGGCTCCCTCTCGTGAAGTGTCTTCTCACGGGCTGTGCCTCTCAATCTGGACGTGATGGGTGCTCTGGCCAA
 GGAGGGCGAGCCAGGACGCTCTTCGGCTTCTGTGGCCCTGCACCGGACTTGCACCGCCAGCCAGGAGTCT
 GCTGCTGGTGGGTGCTCCCCAGGCGCTGGCTTCTTCTGGGCGAGCGCGAATTCGCACTGGAGGCTCTTCGCTTG
 CCCGTGTAGCCTGGAGGAGTACTGCTGTACAGAGTGGACATCGACCAAGGAGCTGATATCGAAAGGAAAGCAA
 TGAGAACAGTGGTGGGAGTCAAGTGTTCGAGCGCAGGGGCTCGGGGCAAGATTGTATTCTGTGCACACCGATA
 GGAGCAAGGACGCGAGTGGACAGATCTCGAGACCGCGGATATGATTGTGCTGCTGCTTTGTGCTCAGCGAGGA
 CTTGGCCTATCCGGATGAGTTGGATGTGGGGAATGGAAGTTCTGGGCTGGAGCCCCCGCGCCCAACCA
 TGGTCTTCCGACAGGCGCACGCTGCCCTCCCTCTTCCCTGATAGCCACTACCTCTCTTTGGGGCCCCAGGAAC
 CTATAATTGGAAGCAAGCCAGGCGAGGCTGGAGCTCTGTGTCACAGGGCTCAGCGGACTTGGCACAACCTGGACGACG
 TCCCTACGAGCGCGGGAGAGGAGGAGGAGGACCCCCGCTCATCCCGGTCCCTGCCAAACGCTACTTTGGCTT
 CTCTATTGACTCGGGAAGGCTCTGTGCTGTGTCAGAGAGCTGAGCTTTGTGGCTGGAGCCCCCGCGCCCAACCA
 CAGGGGTGCTGTGCTCATCTCTCGCAAGGACAGCGCCAGTCCCTGTGTCGGCAGGTTATGCTGTCTGGGAGGCG
 CTTGACCTCCGCTTTGGCTACTCACTGGCTGTGGCTGACCTCAACAGTGTGCTGGCTGGCCAGACCTGTATGTTGGG
 TGGCTTCTTCTTTGAGGCGCAAGAGAGCTGGGGGGTGTGTGTATGTGTACTTGAACAGGGGGGTCACTG
 GGCTGGGATCTCCCTCTCCGGCTGTGGCTCCCTGACTCCATGTTCCGGGATCAGCGTGGCTGTCTGCGGGGA
 CTTCAACCAAGATGGCTTCCAGATATTGAGTGGGTGCCCTTTGATGGTGTATGGGAAAGTCTTCACTTACCA
 TGGGAGCAGCTTGGGGTGTGTCGCCAAACCTTCAAGGTGCTGGAGGGGAGGCTTGGGCTCAAGAGCTTCG
 CTACTCCCTGTCAAGGAGCTTGGATATGGATGGGAACCAATACCTGACCTGTGTGGTGGCTTCCCTGGCTGACAC
 CGCAGTGTCTTTCAGGGCCAGAGCCATCTCCATGTCTCCCATGAGGCTCTTATGTCTCCAGAGCATCGACCT
 GGAGCAGCCAACTGTGCTGGCGGCCATCTGGTCTGTGTGGACTAAGGGTCTGTTTTCAGCTACATTGCACTGCC
 CAGCAGCTATAGCCCTACTTCTGGCCCTGGACTATGTGTTAGATGCGGACACAGCGAGGCTCCGGGGCCAGGT
 TCCCGTGTGACGTTCTGTAGCGCTTAACCTGGAAGAACCCAGCAGCAGGCTCCGGGCAACGCTGTGGCTGGAAGCA
 CCCCATCTCAAGCAGTCTTGTGGAGAGCGCCATGTTCCAGCTCCAGGAAATGTCAAAGCAAGCTTCCGGGCTGT
 AGTGACCTTGTCTTACAGTCTCAGACCCCTCGGCTCCGGCGACAGGCTCTTCCGCGAGGGCTCCCTCAGTGGC
 CCCCATCTCAATGCCACCAGCCAGCAGCAGCCAGCGGGCAGAGATCACTTCTGAGAGCAAGGCTGTGGTGAAGA
 CAAGATCTGCCAGAGCAATCTGACGCTGTGCCAGCCCGCTTCTGTACCCGGGCTCAGGCAACCGAATTCCAACT
 TCTGCCCATGGATGGATGGAGTGAACCAACAGCCCTGTTTGCATGAGTGGGCGAGGCTCATTTGGCTGGAGCTGAT
 GGTCAACCACTTGCATCGGACCCAGCCAGCGCCAGGCTGATGGGATGATGCCCATGAAGCCAGCTCTCTGGT
 CATGCTTCTGTGACTCACTGCATCTACTCAGGGGTCCGGGCTTGGACCTCTCGAGAGACCACTCTGCTGTCCAA
 TGAAGATGCTCCCAATGTTGAGTGTGAGCTGGGGAACCCATGAAGAGAGCTGCCAGGTCACTTCTACTCTCAT
 CCTTAGCAGCTCCGGGATCGACATTGAGACACGGAACCTGGAGTGAAGCTGTCTTGGCCAGCATCAGTGAAGCA
 GGAGCTGTCACTGATCTCTGTGACAGAGCCGTGTCTTCAATTGAGCTGCCACTGTCTTGTGGCCAGCATCAGTGAAGCA
 CCAGCAACTCTTCTTCTTGTGTGGTGGAGGGCCAGAGAGCCATGCACTTCCAGGAAATGGCCATTC
 CAAGTATGAGGTACAGGTTTCCAAACAGGCCAGTCCCTCAGAACCTCTGCTGTATCCCAATGCAAGTGTGAGCTGGAGGGCGGCGAGGGCCGTGG
 GCTCATGAGATTGGCCAAATGGGAAGTGGTGTCTGTATCCCAATGCAAGTGTGAGCTGGAGGGCGGCGAGGGCCGTGG
 GCTGAGAGCCACTGTGACGACAGGAGCCCTGGTGAAGCGCAGGAGCCAGCATGTCTTGTGTGCCCATGTTCTCTC
 TGAAGAAAGAAACCACTCACCTTGGACTGCGCCCGGGGACGGCCAACTGTGTGGTGTCTGAGCTGCCCACTCTA
 CAGCTTTGACCGCGCGGCTGTGCTGCATGTCTGGGGCCGTCTGTGAACAGCAGCTTTCTGGAAGAGTACTCAG
 TGTGAAGTCCCTGGAAGTATGTTGCGGGCCAACTACAGTGAAGTCTTCCATAAAGAACTTGATGCTCGAGAGA
 TCCCTTCAAGATCTCCAGTGTGATGTGTATCTTGGACCCCATGGCTGTGGTGTGCGAGAGGATGCCCTGTGGTGGT
 CATCTCTCTGCTGTACTTGGCTGGCTGTGTGCTAGCACTGTGGTGTGCTCTCTGTGGAAGATGGGATTTCTT
 CAAAGCGGCGAAGCAGCCCGAGGCGACCGTGTGCCAGTACCATGCGGTGAAGATTCTCTGGGAAGACCGACAGCA
 GTTCAAGGAGGAGAGACGGGCACTCTGAGGAACAACTGGGCGAGCCCCGGCGGAGGGCCAGCTGACGCA
 CCCCATCTTGGCTGTGAAGCGGCATCCGAGCTGGGCCCCGATGGGCTCCAGGGCCAGGCAACCGCTTGGTCTCC
 CATGTCCAGCCTTGGCTTGTGGCTGGCTCCATCTCTTCCAGAGATGGCTCTTGGGATGAAGAGGTAGAT
 GGGCTGTGCTGTGCTGATCAAGATTTGGCAGGATCGGCTTCTCAGGGGCAAGAGCTTCTCCACCCCAAGAAC
 TCTCCCAACCACTTCCCTTAGAGTGTCTGTGAGATGAGAGTGGGTAAATCAGGACAGGCGCATGGGCTAGGG
 TGAAGAAGGAGGGGTGCTGCTGCAAAAGTGGGAGAGGGATCTTAATCCCTTCTCTTCCCATCAACCTGT
 GTAAAGAGGCCCAAGGCTGTCTCCCGGGAAGTGTCTTAACCTGAGCTCGGGGAGGAGGTGTGTGCTACTGA
 CTCAGGCTGCTCTCTCTAGTTTCCCTCTCATCTGACCTTAGTTTGTGCTGCATCAGTCTAGTGGTTTCTGGT
 TTCGCTATTATTAAATAATTTTGAACAACAAAAAATAAAAAAAAAA

007036-124701

FIGURE 177

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA55737
><subunit 1 of 1, 1141 aa, 1 stop
><MW: 124671, pI: 5.82, NX(S/T): 5
MAGARSRDWPWASGICYLFGSLLVELLFSRAVAFNLDVMGALRKEGEPGSLFGFSVALHRQL
QPRPQSWLLVIGAPQALALPGQQANRTGGLFACPLSLEETDCYRVDIDQAGDMQKESKENQWL
GVSVRSQGGGKIVTCAHRYEARQRVDQILETRDMIGRCFVLSQDLAIRDELDGGEWKFCGE
RPOGHEQFGFCQOGTAAAFSPDSHYLLFGAPGTYNWKG TARVELCAQGSADLAHLLDDGPYEA
GGEKEQDPRLLIPVPANSYFGFSIDSGKGLVRAEELS FVAGAPRANHKGAVVILRKDSASRLV
PEVMLSGERLTSGFGYSLAVADLNSDGWPDLLVIGAPYFFERQBELGGAVVYVLNQGGHWAGI
SPLRLCGSPDSMFGISLAVLGDNLNDGFPDIAVGAPFDGDGKVF IYHGSSLG VVAKPQSVLE
GEAVGIKSPGYSLSGSLDMGDNQYFPDLLVGS LADTAVLFRARPI LHVSHVESIAPRSIDLEQ
PNCAGGHSVCVDLRVCFSYIAVPSSYSPTVALDYVLDA DTDRRLRGQVPRVTFLSRNLEEPK
HQASGTVWLKHQHDRVCGDAMFQLQENVKDKLRAIVVTTLSYSLQTPRLRRQAPQGGLPPVAP
ILNAHQPSQTRAEIHFLKQCGGEDKICQSNLQLVHARFCTRVSDTEFQPLPMDVDGTTALFA
LSGQPVIGLELMVTNLPSDPAQPDAGDDAHEAQLLVMLPDSLHYSGVRALDPAEKPLCLSN
ENASHVECELGNPMKRGAVTFYLLSTSGISIETTELEVVELLATISEQELHPVSARARVF
IELPLSIAGMAIPQQLFSGVVRGERAMQSERDVGSKVKEYEVTVSNGQQLRTLGS AFLNIM
WPHEIANGKWLlyPMQVELEGGQGPGQKGLCSPRPNILHLDVDSDRRRRRELEPPEQQEPEGE
RQEPMSWNPVSSAEKKKNITLDCARGTANC VVFSCLPYSFDRAAVLHVWGRLWNSTFLEEY
SAVKSLLEVIVRANI TVKSSIKNLMLRDASTVIPVMVYLDPM AVVAEGVPWVWVILLAVLAGLL
VLALLVLLWKMGFFKRAKHPEATVPQYHAVKIPREDRQQFKBEKTGTILRNWGS PRREGP
DAHPILAADGHPGLGPDGHPGPETA
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Important features:

Signal peptide:

amino acids 1-33

Transmembrane domain:

amino acids 1040-1062

N-glycosylation sites.

amino acids 86-89, 746-749, 949-952, 985-988 and 1005-1008

Integrins alpha chain proteins.

amino acids 1064-1071, 384-408, 1041-1071, 317-346, 443-465, 385-407, 215-224, 634-647, 85-99, 322-346, 470-479, 442-466, 379-408 and 1031-1047

FIGURE 178

CGCGCCGGGCGCAGGGAGCTGAGTGGACGGCTCGAGACGGCGGCGGTGCAGCAGCTCCAGA
AAGCAGCGAGTTGGCAGAGCAGGGCTGCATTTCCAGCAGGAGCTGCGAGCACAGTGTGGCT
CACAACAAGATGTGCTCAAGGTGTGAGCCGTACTGTGTGTGTGTGCAGCCGCTTGGTGCAGTCA
GTCTCTCGCAGCTGCCGCGGGCGGTGGCTGCAGCCGGGGGGCGGTGCGACGGCGGTAAATTTTC
TGGATGATAAAACATGGCTCACCACAATCTCTCAGTATGACAAGGAAGTCGGACAGTGGAAAC
AAATTCGAGACGAAGTAGAGGATGATTATTTCCGCACCTGGAGTCCAGGAAAAACCCCTTCGA
TCAGGCTTTAGATCCAGCTAAGGATCCATGCTTAAAGATGAAATGTAGTCGCCATAAAGTAT
GCATTGCTCAAGATTCTCAGACTGCAGTCTGCATTAGTCACCGGAGGGCTTACACACAGGATG
AAAGAAGCAGGAGTAGACCATAGGCAGTGGAGGGGTCCCATATTATCCACCTGCAAGCAGTG
CCCAGTGGTCTATCCCAGCCCTGTTTGTGGTTCAGATGGTCATACCTACTCTTTTCAGTGC
AACTAGAATATCAGGCATGTGTCTTAGGAAAACAGATCTCAGTCAAATGTGAAGGACATTGC
CCATGTCCCTTCAGATAAGCCCACCGTACAAGCAGAAATGTTAAGAGAGCATGCAGTGACCT
GGAGTTCCAGGGAAGTGGCAAAACAGATTGCGGGGACTGGTTCAAGGCCCTTCATGAAAGTGGAA
GTCAAAACAAGAAGACAAAAACATTGCTGAGGCCTGAGAGAAGCAGATTTCGATACCAAGCATC
TTGCCAATTTGCAAGGACTCACTTGGCTGGATGTTTAAACAGACTTGATACAAACTATGACCT
GCTATTGGACCACTCAGAGCTCAGAAGCATTACCTTGATAAGAATGAACAGTGTACCAAGG
CATTCTTCAATTCTTGTGACATACAAGGACAGTTTAATATCTAATAATGAGTGGTGTCTAC
TGCTTCCAGAGACAGCAAGACCCACCTTGCCAGACTGAGCTCAGCAATATTCAGAAGCGGCA
AGGGGTAAAGAAGCTCCTAGGACAGTATATCCCCCTGTGTGTGACAGATATGGAATGTTACTACAAGC
CAACACAATGTCTATGCGAGTGTGGACAGTGTGGTGTGTGACAGATATGGAATGGAATG
ATGGGATCCAGAATAAATGGTGTGTGAGATTGTGCTATAGATTTTGAGATCTCCGAGATTT
TGCTAGTGGCGATTTTCATGAATGGACTGATGATGAGGATGATGAAGACGATATTATGAATG
ATGAAGATGAAATTGAAGATGATGATGAAGATGAAGGGGATGATGATGATGGTGGTGTGAC
CATGATGTATACATTTGATTGATGACAGTTGAAATCAATAAATCTACATTTCTAATATTTA
CAAAAATGATAGCCTATTTAAATATCTTCTTCCCCAATAACAAAATGATTCTAAACCTCA
CATATATTTTGTATAATTATTTGAAAAATTGCAGCTAAAGTTATAGAATTTATGTTTAAAT
AAGAATCATTTGCTTTGAGTTTTTATATTCCCTTACACAAAAGAAAATACATATGCAGTCTA
GTCAGACAAAATAAAGTTTGAAGTGCTACTATAATAAATTTTTCACGAGAACAACTTTGT
AAATCTTCATAAGCAAAATGACAGCTAGTGCTTGGGATCGTACATGTTAATTTTTTGAAG
ATAATCTAAGTGAAATTTAAATAAATAAATTTTTAATGACCTGGGTCTTAAGGATTTAGG
AAAAATATGCATGCTTTAATTGCATTTCCAAAGTAGCATCTTGCTAGACCTAGATGAGTCAG
GATAACAGAGAGATACCATGACTCCAAAAAAAAAAAAAAAA

FIGURE 179

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49829
><subunit 1 of 1, 436 aa, 1 stop
><MW: 49429, pI: 4.80, NX(S/T): 0
MLKVSAVLCVCAAAWCSQSLAAAAVAAAGGRSDGGNFLDDKQWLTTISQYDKEVGQWNKFR
DEVEDDYFRTWSPGKPFQALDPAKDPCCLKMKCSRHKVCIAODSQTAVCISHRRLTHRMKEA
GVDHRQWRGPILSTCKQCPVVYPSPVCGSDGHTYSFQCKLEYQACVLGKQISVKCEGHCCPCP
SDKPTSTSRNVKRACSDLEFREVANRLRDWFKALHESGSQNKTKTLLRPERSRFDTSILPI
CKDSLGMWFMRLDTNYDLLDQSELRSIYLDKNEQCTKAFFNSCDTYKDSLISNNEWCYCFQ
RQQDPPCQTELSNIQKRQGVKKLLGQYIPLCDEDDGYKPTQCHGSVGCWCVDRYGNEVMGS
RINGVADCAIDFEISGDFASGDFHEWTDDEDDIMNDEDEIEDDDEDEGDDDDGGDDHDVYI

Important features:

Signal peptide:

amino acids 1-16

Leucine zipper pattern.

amino acids 246-267

N-myristoylation sites.

amino acids 357-362, 371-376 and 376-381

Thyroglobulin type-1 repeat proteins

amino acids 353-365 and 339-352

FIGURE 180

CAGACTCCAGATTTCCTGTCAACCACGAGGAGTCCAGAGAGGAAACGCGGAGCGGAGACAAACAGTACCTGACGC
 CTCTTTACGCCCGGGATCGCCACGACAGGAGATGGGCGCACAAGATCTGGCTGCCCTTCCCGCTGCTCTTCTGGCC
 GCTCTGCCCTCGGCTGCTGCTGCCCTGGGGCGCGGCTTTCACACTTCCCTCGATAGCAGTCTCACCTTACCTTT
 CCCGCGCGGCAGGAAGAGTGTCTTACCAGCCCATGCCCCGTAAGGCCCTCGCTGAGATCGACTGATACCAAGTTTAA
 GATGGAGCAGGATTAGATATGATTGATTCCATCTTGCTCTCCAGAAGGCAAACTTAGTTTGTGAACAAAGAAAA
 TCGATGGAGTTCACACTGTAGAGACTGAAGTTGGTGATTACATGTTCTGCTTTGACAAATACATTTCAGCACCAATT
 TCTTGAGAAGGTGATTTTCTTTGAATTAACTTCCCTGCTGATGAACTGGAAGACATCTGGGATTCATCAACAGCATCAAGTCC
 AAATATATATCTGGCCACAGATATATGGATATGAACTGGAAGACATCTGGGATTCATCAACAGCATCAAGTCC
 AGACTGAACAAAGTGGCCACATCAAAATTCTGCTTAGAGCATTTGAAGTCTGCTGATCGAAACATACAGAAAGC
 AACTTGTATAGACTCAATTTCTGGTCTATGGTTAAATTAGTGGTCTGGTGGTGGTGCAGCCATTCAAGTTTAT
 ATGCTGAAGAGTCTGTTTGAAGATAAGAGGAAAGTAGAATCTAAACTCCAACTAGAGTACGTAACTTGA
 AATAGGCGATAAAATGCAATAAACTGTTACAGTCAAGACCATTAATGGTCTTCTCCAAATATTTTGAGATATA
 AAAGTAGGAAACAGGTATATTTTAAATGTGAAATTAAGTCTTCACTTTCTGTCGAAGTAACTCTGCTGATCCAG
 TTGCTACTTAAGTGTGTAACAGGAATATTTTGCAGAAATAGGTTTAACTGAATGAAGCCATATTAATAACTGCAT
 TTCTCTAACCTTTGAAAAATTTTGCAAATGTCTAGGTGATTTAAATAAAGAGTATTTGGGCTTAATGCAACACC
 AGTCTGTTTAAACAGGTTCTATTACCCAGAACTTTTGTAAATGCGGCAGTTACAAATTAACGTGGAAAGTTT
 TCGATTTTTAAGTTATAAATCACCTGAGAATTACCTAATGATGGATTGAATAAATCTTTAGACTACAAAGCCCAAT
 TTTCTCTTCTATTACATATGTCATCTCTCTATAATGTAATAGATAATAGCTTTTGAATAACAATTAGGTTTGTG
 AGATTTTATAACCAAAATACATTTTCAGTGTAAACATATTAGCAGAAAGCATTAGTCTTTGTATCTTGCTTACATTC
 CCAAAGCTGACATTTTCAGATTCTTAAAAACACAAAGTTACACTTAACTAAATTAAGGACATGTTTCTCTTTG
 AAATGAAGAATAAGTTTAAAGCTTCTCTCTCCATAGGGACACATTTTCTTAACCTCTAACTAAAGTGTAGGA
 TTTTAAATTAATGTGAGGTAATAAGTTTATTTTAAATAGTATCTGTCAAGTAAATATCTGTCAACAGTTAA
 TAATCATGTTATGTTAAATTTTACATGATTGCTGACTTGGATAATCTATTATCTACAGCAGTTATGAAGGAAATA
 TTGCTAAATGATCTGGGCTACCATAAATAAATATCTCTTTCTGAGCTCTAAGATCTCTGTTATCAGAAACAGGAA
 AGAATTTAGAAAACTTGAGAAAACTTAATCCAAAAATAAATTCACCTTAAGTAGAACTATAAATAAATCTAGAA
 ATCTGACTGGCTCATCATGACCTCTACTCTATAACATAAATCAAAGGAGATGATTAATTTCCAGTTAGCTGGAAG
 AAACTTTGGCTGTAGGTTTTCATTTTCTCAAGAAATCTGGTTTGAATTAATTTTGTGAAGCGATCATTTTATA
 AAATGTAAGCCCTACTGTAAGGTTTAGCACTGGGTGTACATATTATTAATAAATTTTATTATAACAACTTTTAT
 TAAATGGCCCTTTCTGAACACTTATTATTATGATGTTGAAGTAAGGATAGAAACATAGACTCCCAAGTTTAAAA
 CACCTAAATGTGAATAACCCATATATAACAACAAAGTTTCTGCCATCTAGCTTTTGAAGTCTATGGGGTCTTAC
 TCAAGTACTAGTAAATTAATCTCATCATGAATGAACATAAATTTTAAAGTATGCCCCATTATAACGCTGTTTAT
 GACTACATTTGTGAGTTAGAAACAACTTAAATTTGGGGTATAGAACCCCTCAACAGGTATGTAATGCTGGAATT
 CTGTGATGAGCAATAATGATAACAGAGAGTGAATTCATTACACTCATAGTAGTATAAAAGAGATACATTTCCCC
 TCTTAGGCCCTGGGAGAGAGAGAGTCTTAGATTCCCTACTGGCAAGGTTTAAAAATGAGGTAAATGCGGTAT
 ATGATCAATTAACCTTAATTTGGCCAGGAAATGCTTCAGGTGTCTAGGGGTATCCCTGCGACACATTCGCAACAA
 AGGTCAATAAGATCTTGGCTATGTAATACCCCTCCCTTTTGGCGTGTAAATTTGCAATGAGAAGCAAAATTTACA
 GTACCAATCAATAAAGCAGGGTACAGATATAAACTACTGCATCTTTCTATAAAATCTGATTAAGAATTTCTA
 CCTCTCTGTGTGGTGTACTGTACTGTACTCTGTACTCTTACCTAACCAATGAATTTGTTACATAATCTTCT
 ACATGTATGATTTGGCCACTGATCTTAAACCTATGATTGATGATTAATCTTACCATATAAAACGATAATGCTCT
 TATTGGAAGAAAGTATTAAGAACTACTAAGGACAATTAATTTTATAGACAAAGTAAAAAGACAGATATTTAAGAGG
 CATAAACAAAAAGCAAACTGTGAACAGAGTAAAAATCTTAAATTTCTTAAAGACATCTGTTTATCTGCTT
 CATATGCTTTTGTATTTTCACTATTTCCATTTCTAAATTAAGTATGCTAAATTTGATTAAGCTGTTTATCACTT
 AACAGCTCAATTTTGTCTTTTCAATATACAAATTTTAAAAATACATAATTTTAACTAAGGCCCAACCGATTTC
 CATATGTAGCAGTTACCGTGTTCACCTCACATAAGGCCCTAGAGTTTGTCTGTATGATGATTTGATGATTAAT
 GTTATGCTGTTCTTCTCATGTGAATGTCAAGACATGGAGGGTGTGTTGAATTTTATGTTAAAAATTAATCTTCTA
 CACATAATGCTGTCTTAAATGTGACAAAAATGAGCACATTAATTTGATGCTCTCTCAATTAAGATTTCTTTAT
 GTGAAATTTTAAAGACATTTGATCTGAGTGAAGGATTTTCTCTGAGTGAACATAATGAGCACAACTGAGTGTG
 CTCAAACTGCTTTTATCTATTAACAGCCATCTTAAATAAGCAACGATTTGTGAGTACTGATATGATATAATAA
 AAATTTCAAGAGAAAA

1007066-102401

FIGURE 181

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52196
><subunit 1 of 1, 229 aa, 1 stop
><MW: 26017, pI: 4.73, NX(S/T): 0
MGDKIWLPPFVLLLAALPPVLLPGAAGFTPSLSDSDFFTLPAGQKECFYQPMPLKASLEIEY
QVLGDAGLDIDFHLASPEGKTLVFEQRKSDGVHTVETEVGDYMFCDNTFSTISEKVIFFEL
ILDNMGEQAQEQEDWKKYITGTDILDMKLEDILESINSIKSRLSKSGHIQILLRAFEARDN
IQESNFDVRVNFWSMVNLVVMVVVSAIQVYMLKSLFEDKRKSRT

Important features:

Signal peptide:

amino acids 1-23

Transmembrane domain:

amino acids 195-217

N-myristoylation site.

amino acids 43-48

Tyrosine kinase phosphorylation site.

amino acids 55-62

FIGURE 182

CCATCCCTGAGATCTTTTATAAAAAACCCAGTCTTTGCTGACCAGACAAAGCATACCAGAT
CTCACCAGAGAGTCGCAGACACTATGCTGCCTCCCATGGCCCTGCCAGTGTCTCTGGATG
CTGCTTTCCTGCCTCATTCTCCTGTGTGTCAGGTTCAAGGTGAAGAAACCCAGAAGGAAGTCCC
CTCTCCACGGATCAGCTGTCCCAAAGGCTCCAAGGCCTATGGCTCCCCCTGCTATGCCTTGT
TTTTGTACCAAAATCCTGGATGGATGCAGATCTGGCTTGCCAGAAGCGGCCCTCTGGAAAA
CTGGTGTCTGTGCTCAGTGGGGCTGAGGGATCCTTCGTGTCTCCTGGTGAGGAGCATTAG
TAACAGCTACTCATACATCTGGATTGGGCTCCATGACCCACACAGGGCTCTGAGCCTGATG
GAGATGGATGGGAGTGGAGTAGCACTGATGTGATGAATTACTTTGCATGGGAGAAAAATCCC
TCCACCATCTTAAACCTGGCCACTGTGGGAGCCTGTCAAGAAGCACAGGATTTCTGAAGTG
GAAAGATTATAACTGTGATGCAAAGTTACCTATGTCTGCAAGTTCAAGGACTAGGGCAGGT
GGGAAGTCAGCAGCCTCAGCTTGGCGTGCAGCTCATCATGGACATGAGACCAGTGTGAAGAC
TCACCCTGGAAGAGAATATTCTCCCAAAGTGCCTTACCTGACTACCTTGTGATGATCCTCC
TTCTTTTCTTTTCTTTCACCTTCATTTTCTGCTCTTCCATGTCTTGAGATC
TCAGAGAATAATAAAAAATGTTACTTTATAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 183

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56965

<subunit 1 of 1, 175 aa, 1 stop

<MW: 19330, pI: 7.25, NX(S/T): 1

MLFPMALPSVSWMLLSCLILLCQVQGEETQKELPSPRISCPKGSKAYGSPCYALFLSPKSWM
DADLACQKRPSGKLVSVLSGAEGSFVSSLVRSISNSYSYIWIGLHDPTQGSEPDGDGWEWSS
TDVMNYFAWEKNPSTILNPGHCGSLSRSTGFLKWKDYNCDAKLPYVCKFKD

Important features:

Signal peptide:

amino acids 1-26

C-type lectin domain signature.

amino acids 146-171

FIGURE 184

CCAGTCTGTGCGCCACCTCACTTGGTGTCTGCTGTCCCCGCCAGGCAAGCCTGGGGTGAGAGC
ACAGAGGAGTGGGCGGGGACCATGCGGGGGACGCGGCTGGCGCTCCTGGCGCTGGTGTCTGGC
TGCCTGCGGAGAGCTGGCGCCGGCCCTGCGCTGCTACGTCTGTCCGGAGCCACAGGAGTGT
CGGACTGTGTCACCATCGCCACCTGCACCACCAACGAAACCATGTGCAAGACCACACTCTAC
TCCCGGGAGATAGTGTACCCCTTCCAGGGGGACTCCACGGTGACCAAGTCCTGTGCCAGCAA
GTGTAAGCCCTCGGATGTGGATGGCATCGGCCAGACCCGCCCCGTGTCCTGTGCAATACTG
AGCTGTGCAATGTAGACGGGGCGCCCGCTCTGAACAGCCTCCACTGCGGGGCCCTCACGCTC
CTCCCACTCTTGAGCCTCCGACTGTAGAGTCCCCGCCACCCCATGGCCCTATGCGGCCCA
GCCCCGAATGCCTTGAAGAAGTGCCCCCTGCACCAGGAAAAAAAAAAAAAAAAA

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FIGURE 185

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56405

<subunit 1 of 1, 125 aa, 1 stop

<MW: 13115, pI: 5.90, NX(S/T): 1

MRGTRLALLALVLAACGELAPALRCYVCPEPTGVSDCVTIATCTTNETMCKTTLYSREIVYP
FQGDSTVTKSCASKCKPSDVDGIGQTLFVSCCNTELCNVDGAPALNSLHCGALTLLPLLRL

Important features:

Signal peptide:

amino acids 1-17

N-glycosylation site.

amino acids 46-49

FIGURE 186

CTGCAGTCAGGACTCTGGGACCGCAGGGGGCTCCCGGACCCCTGACTCTGCAGCCGAACCGGC
ACGGTTTCGTGGGGACCCAGGCTTGCAAAGTGACGGTCATTTTCTCTTTCTTTCTCCCTCTT
GAGTCCTTCTGAGATGATGGCTCTGGGCGCAGCGGGAGCTACCCGGGTCTTTGTGCGGATGG
TAGCGCGGCTCTCGGCGGCCACCCTCTGCTGGGAGTGAGCGCCACCTTGAACTCGGTCTC
AATTCCAACGCTATCAAGAACCTGCCCCACCGCTGGGCGGCGCTGCGGGGCACCCAGGCTC
TGCAGTCAGCGCCGCGCCGGGAATCCTGTACCCGGGCGGGAATAAGTACCAGACCATTGACA
ACTACCAGCCGTACCCGTGCGCAGAGGACGAGGAGTGCGGCCTGATGAGTACTGCGCTAGT
CCCACCCGCGAGGGGACGCAAGCGTGCAAATCTGTCTCGCCTGCAGGAAGCGCCGAAAACG
CTGCATGCGTCACGCTATGTGCTGCCCGGGAATTACTGCAAAAATGGAATATGTGTGTCTT
CTGATCAAAATCATTTCCGAGGAGAAATTGAGGAAACCATCACTGAAAGCTTTGGTAATGAT
CATAGCACCTTGGATGGGTATTCCAGAAGAACCACCTTGTCTTCAAAAATGTATCACACCAA
AGGACAAGAAGGTTCTGTTTGTCTCCGGTCATCAGACTGTGCCTCAGGATTGTGTTGTGCTA
GACACTTCTGGTCCAAGATCTGTAAACCTGTCTGAAAGAAGGTCAAGTGTGTACCAAGCAT
AGGAGAAAAGGCTCTCATGGACTAGAAATATTCACGCGTGTGTTACTGTGGAGAAGGTCTGTC
TTGCCGGATACAGAAAGATCACCATCAAGCCAGTAATTTCTTAGGCTTCACTTGTGCAGA
GACACTAAACCAGCTATCCAAATGCAGTGAACCTCTTTTATATAATAGATGCTATGAAAACC
TTTTATGACCTTCATCAACTCAATCCTAAGGATATACAAGTTCTGTGGTTTCAGTTAAGCAT
TCCAATAACACCTTCCAAAACCTGGAGTGTAAAGGCTTTGTTTCTTTATGGAACCTCCCCTG
TGATTGCAGTAAATTACTGTATTGTAAATTCTCAGTGTGGCACTTACCTGTAAATGCAATGA
AACTTTTAATTATTTTCTAAAGGTGCTGCACTGCCTATTTTTCTCTTGTGTATGTAAATTT
TTGTACACATTGATTGTTATCTTGACTGACAAATATTCTATATTGAACTGAAGTAAATCATT
TCAGCTTATAGTTCTTAAAAGCATAACCCCTTTACCCCATTTAATTCTAGAGTCTAGAACGCA
AGGATCTCTTGAATGACAAATGATAGGTACCTAAAATGTAACATGAAAATACTAGCTTATT
TTCTGAAATGTACTATCTTAATGCTTAAATTATATTCCCTTTAGGCTGTGATAGTTTTTGA
ATAAAATTTAACATTTAAAAA

FIGURE 187

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57530

<subunit 1 of 1, 266 aa, 1 stop

<MW: 28672, pI: 8.85, NX(S/T): 1

MMALGAAGATRVFVAMVAAALGGHPLLGVSATLNSVLNSNAIKNLPPPLGGAAGHPGSAVSA
APGILYPGGNKYQTIIDNYQYPYCAEDECCTDEYCASPTRGGDAGVQICLACRKRKRKCMRH
AMCCPGNYCKNGICVSSDQNHFRGEIETITESFGNDHSTLDGYSRRTTLSSKMYHTKGQEG
SVCLRSSDCASGLCCARHFWSKICKPVLKEGQVCTKRRRKGSHGLEIFQRCYCGEGLScriQ
KDHQASNSSRLHTCQRH

Important features:

Signal peptide:

amino acids 1-23

N-glycosylation site.

amino acids 256-259

Fungal Zn(2)-Cys(6) binuclear cluster domain

amino acids 110-126

[illegible]

TGTGTTTCCCTGCAGTCAGAAATTGGGACNGCAGGGGTTCCCGGACCTGATTTTGCACGCGA
ACGGGAAGGTTTTGTGGGACCCAGGTTGAAATGACGGTCATTTTTTTTCTTCTCCTTCNG
GAGTCCTTNTGAGANGATGTTTTGGGCGCAGCGGGAGCTAACCCCGTTTTTTGTNGCGATG
GTAGCGGCGGTTTTTCGGCGGCCACCTTNTGCTGGGAGTGAGCGCCACCTTGAATCGGTTTTTC
AATTCCAACGNTATCAAGAACCTGCCCCACCGNTGGGCGGCGCTGCGGGGCACCCAGGNTT
TGCAGTCAGCGCCGCGCCGGGAATCCTGTACCCGGGCGGGAATAAGTACCAGACCATTGACA
ATTACCAGCCGTACCCGTGCGCAGAGGACGAGGAGTGCGGCACTGATGAGTACTGCGCTAGT
CCCACCCGCGGAGGGGATGCGGCGTGCAAAATNTGTTNTNGCCTGCAGGAAGCGCCGAAAAACG
CTGCATCGCCTCANGCTATGTGCTGCCCGGGGAATTACTGCAAAAATGGAATATGTGTGTTNT
CTGATCAAAATCATTTCCGAGGAGAAATTGAGGAAACCATCACTGAAAGCTTTGGTAAATGAT
CATAGCACCTTGGATGGG

FIGURE 189

GAGGAACCTACCGGTACCGGCCGCGCGCTGCTAGTGC CGCGGTGGCTGCACCTCACCAATCCCCTGCGCCCGCG
 CTGGCCGCTCGGAGAGTGCCTGTCTCTCTCTGCACCGCGTCTGGGCTCGGCCAGGCCGGGTCCGCCGCCA
 GGGTTTGAGGATGGGGGATAGCTACAGGAAGCGACCCCGGATGGCAAGGTATATTTTGTGGAATGAAAGGA
 AGTATTAGAAATGAGCTGAAGACCATTCACAGATTAAATTTTGGGGACAGATTTGTATGCTTGATCCCTCT
 TGAAGTAATGTAGACAGAAGTTCTCAAAATTTGCATATACATCAACTGGAAACGAGCAGTGAATCTTAATGTTAC
 TAAATCGGAACTTGCATAGAAGAGAGATGCGAGCTCGTTTAAATAAAGATGACATATCAGAGACTTGAAAG
 GATCATTTCTGTTTCTGATAGTGTATATGGCCATTTTAGTGGGCACAGATCAGGATTTTACAGTTTACTTTG
 AGTGTCCAAACTCGAAGCAGTAGAGAAATAAGCAAGCTTTCAAGAAATTGGCATTTGAAGTTACATCCTGATAA
 AAACCCGGAATACCCAAATGCACATGGCGATTTTAAATAAATAAGAGCATTAAGTACTCAAAGATGAGA
 TCTACGGAAAAAGTATGACAAATATGGAGAAAGGGACTTGAGGATAATCAAGTGGCCAGATGAAAGCTGGAA
 CTATATTGTTATGATTTTGGTATTTATGATGATGATCCTGAAATCATACATTTGGAAGAAGAGAAATTTGATGC
 TGCCTGTTAATTCTGGAGAACTGTGGTTTGTAAATTTTACTCCCGAGGCTGTTACACATGCCATGATTTAGCTCC
 CACATGGAGAGACTTTGCTAAAGAGTGGATGGGTTACTCGAATGGAGCTGTTAACTGGTGATGATAGAAT
 GCTTTGCCAATGAAAGGAGTCAACAGCTATCCCACTCTCTTCAATTTTCGGTCTGGAATGGCCCGAGTGAATA
 TCATGGAGACAGATCAAAGGAGATTTAGTGAATTTTGAATGCAGCATGTTAGAAGTACAGTGACAGAACTTTG
 GACAGGAAATTTTGTCACTCCATACAACTGCTTTTGTGCTGCTGTTAGTGGCTGGCTGATCACTTTTGTTCAAA
 AGGAGAGATGATTTTGACTTCACAGACAGCATCAGGCTTAGTGGCATGTTGTTTCTCAACTCATGGATGCTAA
 AGAAATGATTTTGAAGATTAATCAATCTTCCAGATTTTGAATCACTTTTCGGCAACACATAGGAGATCGTTT
 GGCATCATCGTGGCTGTTATTTTTCATTTTGGAAAAATGAAATTTCAATGATCTCTGAGCTGAAAAAATCT
 AAAAATCTACTTAAAAATGATCATATTCAGTTGGCAGGTTTGACTGTTCTCTGACCGACAGATCTGTAGTAA
 TCTGATGTTTTCAGCGCTCTCTAGCAGTATTTAAAGGACCAAGGAACCAAGAATATGAATTCATCATGGAAA
 GAGAGTTCTATATGATATCTACTGCTTTTGCACAAAGAGTGTGAATTTCTGTTTACACCGCTGGAGCTCAAAA
 TTTTCTGCCAATGACAAAGAACCATGGCTGTTGATTTCTTGGCCCCCTGGTGTCCACATGCTGAGCTTTACT
 ACCAGATTTACGAAGAGCTCAATCTTCTTTATGGTCAGCTTAAAGTTGGTACATGATTTGACAGTTCATGA
 GGAATCTGTAAACATGTATAACATTCAGGCTTATCCAAACACAGTGTATTAACACCTCCCAAGTTCATGAGTA
 TGAAGCAGATCATCTGCTGGAACAAATCTTGGAGTTCATAGAGGATCTTATGATCTCTAGTGGCTTCCCTTAC
 ACCCACCCCTTCAACGACTAGTTACACAAAGAAAACACAGAGATCTGATGTTGATTTCTATTTCTCGGT
 GTGTCTCTCTGCCAAGCTTAAAGTCTGAGAAATGGAAAGAAATGGCCGACATTAATCGCATGATCAACGTGGG
 CAGTATAGATTCGCCACATATCATCTCTTTTGTGCCAGGAAAACGTTCAAAGATACCTCGAGATGAAGATTTT
 TCCCCAAAATCAAAATAAGCTTATCAGTATCAAGTTACAATGTTGGAAATAGGAGTCTTATCTCTGAGAAT
 CTGGGCTCTAGATTTTATCTCAAGTATCCAGATCTAACACCTCAGACTTTCTAGTGAACAAAGTTCTCAAGG
 GAAATCATGTCGCTGATGATTTCTATGCTCTTGGTGTGGACCTTCCGCAATTTTGTCCAGAAATTTGAGCT
 CTGCTAGGATGATTAAGGAAAAAGTGAAGCTGGAAGATGAGACTGTCAAGGCTTATGCTCAGACATGCCAGAA
 AGCTGGGATCAAGGCTATCCACTGTTAAGTTTATTTCTACGAAGAGCAAGAGAAATTTTCAAGAGAGGAC
 GATAAATCCAGAGATGCAAAAGCAATCGCTGCCTTAATAGTGAAGAAATTTGGAAATCTCCGAAATCAAGGCA
 GAGGAATAGGATGAATTTGATAGATTTGAAGATGAAGAAAAAGTTTAAAAAGAAATTTGACAGATGACATCAG
 AAGACACCTATTAGAAATGTTACATTTATGATGGGAATGAATGAACATTTCTAGACTTGCAGTTGATCGCCA
 GAATTTATCTACAGCATCGTGTAAAGAGAGGCTCTGCAACTTTTCTGTAAAGGGCCGGTTTATAAATATTTT
 GACTTTGACGCTATAATATATGTTTACACATGAGAAACAGAAATAGAGTCAATGATCTTTGTTATTTGCT
 TTTAAACACCTTTTAAAAAATTTAAAAAGATTCTTAGCTCAGAGCCATACAAAGTAGGCTGGATTCAGTCCATG
 GACCATAGATGCTGTCCCCCTCGACCGGATTAATAGTTTTCAGTGGCTGGCTTGAACATGAGTCTGCTGTGCT
 ATCTACATAAATGTTCAAGTTGTATAAAGTCCACTTTCCTTCACTGTTTTCGCTGACCTGAAAGAGGATTA
 TAGTTTGTGTTGCTGCTTCTTCTTAAAAATGCTATCCTTAACCATATATTTATATTTTGTGTTTAAAAACCCAT
 GATGTGGCACAGTAAACCAACCTGTTATGCTGTATTTATGAGGAGATCTTCAATGTTTCTTCTCTCTCA
 AAGGTTGAAAAAATGCTTTTAAATTTTTCACAGCCGAGAAACAGTGCAGCAGTATATGTGCACAGATGAAGTAC
 AAATTTGAGCAACAGTAAGTGCACAAATTTCTGATTTGCTGTATCATCCAGAAAACTGAGGAGAAAAAATTA
 TAGCAATTAAGTGGGATGTTAGAGTATCCTAAATATGTTATCAAGTATTAGAGTTCTATATTTAAAGATATA
 TGTGTTCTAGTATTTTCTGAAATGCTTTTATAGAAATTTTCCACTGATAGTGTGATTTTGTAGGCAATCTAATAT
 TTACATATTTGCTCTGAACTTTGTTTTCAGCTGTATCCTTATTTACATGGTGTCTTTCTTCTATGTTTGTG
 TTTTCTCACTCTGCTGAGTCTATTTATATTCAATAGGAAAAATTACTTTACAGGTTGTTTTCATGAGCTTAT
 ATGATACCTGTAGTTATTCAGGTTACTAGTTTACTGTGACAGGGCTGCTTTTTCAGATAAATATGACATATA
 ACTGAAGTATTTTATAAGAAATCAAGTATATAAATCTAGGAAAGGATCTTCTAGTTTCTGTTGTTTGA
 CTAAGAGATCAAAATTTGTCAGTAACTGATGTTGTTTGTATATAATTCAGAGTTACAGAAATGTAATAAT
 CCAATCAGTCAAAAGAGGCTCAATGAATTAAGAGGCTTGCACCTTTTCAAAAAAATAAAAAA

FIGURE 190

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56439
<subunit 1 of 1, 747 aa, 1 stop
<MW: 86127, pI: 7.46, NX(S/T): 2
MGVWLNKDDYIRD LKRIILCF L I V Y M A I L V G T D Q D F Y S L L G V S K T A S S R E I R Q A F K K L A L K L
H P D K N P N N F N A H G D F L K I N R A Y E V L K D E D L R K K Y D K Y G E K G L E D N Q G G Q Y E S W N Y Y R Y D F G I
Y D D D P E I I T L E R R E F D A A V N S G E L W F V N F Y S P G C S H C H D L A P T W R D F A K E V D G L L R I G A V N C
G D D R M L C R M K G V N S Y P S L F I F R S G M A P V K Y H G D R S K E S L V S F A M Q H V R S T V T E L W T G N F V N S
I Q T A F A A G I G W L I T F C S K G G D C L T S Q T R L R L S G M L F L N S L D A K E I Y L E V I H N L P D F E L L S A N
T L E D R L A H H R W L L F F H F G K N E N S N D P E L K K L T L L K N D H I Q V G R F D C S S A P D I C S N L Y V F Q P
S L A V F K G Q G T K E Y E I H H G K K I L Y D I L A F A K E S V N S H V T T L G P Q N F P A N D K E P W L V D F F A P W C
P P C R A L L P E L R R A S N L L Y G Q L K F G T L D C T V H E G L C N M Y N I Q A Y P T T V V F N Q S N I H E Y E G H H S
A E Q I L E F I E D L M N P S V V S L T P T T F N E L V T Q R K H N E V W M V D F Y S P W C H P C Q V L M P E W K R M A R T
L T G L I N V G S I D C Q Q V H S F C A Q E N V Q R Y P E I R F F P P K S N K A Y Q Y H S Y N G W N R D A Y S L R I W G L G
F L P Q V S T D L T P Q T F S E K V L Q G K N H W I D F Y A P W C G P C Q N F A P E F E L L A R M I K G K V K A G K V D C
Q A Y A Q T C Q K A G I R A Y P T V K F Y F Y E R A K R N F Q E E Q I N T R D A K A I A A L I S E K L E T L R N Q G K R N K D E L
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Important features:

Endoplasmic reticulum targeting sequence.

amino acids 744-747

Cytochrome c family heme-binding site signature.

amino acids 158-163

Nt-dnaJ domain signature.

amino acids 77-96

N-glycosylation site.

amino acids 484-487

FIGURE 191

AGACAGTACCTCCTCCCTAGGACTACACAAGGACTGAACCAGAAGGAAGGACAGAGCAAA
GCCATGAACATCATCCTAGAAATCCTTCTGCTTCTGATCACCATCATCTACTCTACTTGGAG
GTCTGTTGGTGAAGTTTTTTCATTCTCTCAGAGGAGAAAATCTGTGGCTGGGGAGATTGTTCTCA
TTACTGGAGCTGGGCATGGAATAGGCAGGCAGACTACTTATGAATTTGCAAAACGACAGAGC
ATATTGGTTCTGTGGGATATTAATAAGCGCGGTGTGGAGGAACTGCAGCTGAGTGCCGAAA
ACTAGGCGTCACTGCCCATGCGTATGTGGTAGACTGCAGCAACAGAGAAGAGATCTATCGCT
CTCTAAATCAGGTGAAGAAAGAAGTGGGTGATGTAACAATCGTGGTGAATAATGCTGGGACA
GTATATCCAGCCGATCTTCTCAGCACCAAGGATGAAGAGATTACCAAGACATTTGAGGTCAA
CATCTAGGACATTTTTGGATCACAAAAGCACTTCTTCCATCGATGATGGAGAGAAATCATG
GCCACATCGTCACAGTGGCTTCAGTGTGCGGCCACGAAGGATTTCCTTACCTCATCCCATAT
TGTTCAGCAAAATTTGCCGTGTGTGGCTTTCACAGAGGTCTGCATCAGAACTTCAGGCCTT
GGGAAAAAATCGGTATCAAAACCTCATGTCTCTGCCAGTTTTTGTGAATACTGGGTTCACCA
AAAAATCCAAGCACAAGATTATGGCCTGTATTGGAGACAGATGAAGTCGTAGAAGTCTGATA
GATGGAATACTTACCAATAAGAAAATGATTTTTGTTCATCGTATATCAATATCTTTCTGAG
ACTACAGAAGTTTCTTCTGAACGCGCCTCAGCGATTTTAAATCGTATGCAGAATATTCAAT
TTGAAGCAGTGGTTGGCCACAAAAATCAAAATGAAATGGAATAAATAAGCTCCAGCCAGAGATG
TATGCATGATAATGATATGAATAGTTTCGAATCAATGCTGCAAGCTTTATTTCACATTTTT
TCAGTCTTGATAATATTA AAAACATTGGTTTGGCACTAGCAGCAGTCAAACGAACAAGATTA
ATTACCTGTCTTCCCTGTTTCTCAAGAATATTTACGTAGTTTTTCATAGGCTGTGTTTTCTT
TCATGCCTCTTAAAAAATCTGTGCTTACATAAACATACTTAAAGGTTTTCTTTAAGATAT
TTTATTTTTCCATTTTAAAGGTGGACAAAAGCTACCTCCCTAAAAGTAAATACAAAGAGAACT
TATTTACACAGGGAAGGTTTTAAGACTGTTCAAGTAGCATTCCAATCTGTAGCCATGCCACAG
AATATCAACAAGAACACAGAAATGAGTGCACAGCTAAGAGATCAAGTTTCAGCAGGCAGCTTT
ATCTCAACCTGGACATATTTTAAAGATTGAGCATTGAAAGATTTCCCTAGCCTCTTCTTTTT
TCATTAGCCCCAAACGGTGCAACTCTATTCTGGACTTTATTACTTGATTCTGTCTTCTGTAT
AACTCTGAAGTCCACCAAAGTGGACCCTCTATATTTCCCTCCCTTTTTATAGTCTTATAAGA
TACATTATGAAAGGTGACCGACTCTATTTTAAATCTCAGAATTTTAAAGTTCTAGCCCCATGA
TAACCTTTTTCTTTGTAATTTATGCTTTTCATATATCCTTGGTCCCAGAGATGTTTGAACAAT
TTTAGGCTCAAAAATTAAGCTAACACAGGAAAAGGAACTGTACTGGCTATTACATAAGAAA
CAATGGACCCAAGAGAAGAA

FIGURE 192

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56409

<subunit 1 of 1, 300 aa, 1 stop

<MW: 33655, pI: 9.31, NX(S/T): 1

MNIILEILLLLITIIYSYLESLVKFFIPQRRKSVAGEIVLITGAGHGIGRQTTFEFAKRQSI
LVLWDINKRGVEETAACRKLGVTAHAYVVDCSNREEIYRSLNQVKEVGDVTIVVNNAGTV
YPADLLSTKDEEITKTFEVNILGHFWITKALLPSMMERNHGHIVTVASVCGHEGIPYLIPYC
SSKFAAVGFHRGLTSELQALGKTGIKTSCLCPVVFVNTGFTKNPSTRLWPVLETDEVVRSLLID
GILTNNKMIFVPSYINIFLRLQKFLPERASAILNRMQNIQFEAVVGHKIKMK

Important features:

Signal peptide:

amino acids 1-19

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 30-33 and 58-61

Short-chain alcohol dehydrogenase family protein

amino acids 165-202, 37-49, 112-122 and 210-219

FIGURE 193

CGGCGGCGGCTGCGGGCGCAGGTGAGGGGCGCGAGGTGAGGGGCGCGAGGTTCCACGACAGG
ATGCCCGGCTCTGCAGGAAGCTGAAGTGAGAGGCCCGGAGAGGGCCCAGCCCGCCCGGGGC
AGGATGACCAAGGCCCGGCTGTTCGGCTGTGGCTGGTGCTGGGGTCGGTGTTTCATGATCCT
GCTGATCATCGTGTACTGGGACAGCGCAGGCGCCGCGCACTTCTACTTGCCACAGTCCTTCT
CTAGGCCGCACACGGGGCCCGCTGCCACGCGCCGGGCCGGACAGGGACAGGGAGCTCACG
GCCGACTCCGATGTCGACGAGTTTCTGGACAAGTTTCTCAGTGCTGGCGTGAAGCAGAGCGA
CCTTCCAGAAAGGAGACGGAGCAGCCGCCTGCGCCGGGAGCATGGAGGAGAGCGTGAGAG
GCTACGACTGGTCCCCGCGCAGCGCCGGCGCAGCCAGACCAGGCGCGCAGCAGGCGGAG
CGGAGGAGCGTGCTGCGGGGCTTCTGCGCCAACCTCCAGCCTGGCCTTCCCCACCAAGGAGCG
CGCATTCGACGACATCCCCAACTCGGAGCTGAGCCACCTGATCGTGGACGACCGGCACGGGG
CCATCTACTGCTACGTGCCCAAGGTGGCCTGCACCAACTGGAAGCGCGTGATGATCGTGCTG
AGCGGAAGCCTGCTGCACCGCGTGCGCCCTACCGCGACCCGCTGCGCATCCCGCGCGAGCA
CGTGCAACAACGCCAGCGCGCACCTGACCTTCAACAAGTTCTGGCGCCGCTACGGGAAGCTCT
CCCGCCACCTCATGAAGGTCAAGCTCAAGAAGTACACCAAGTTCCTCTTCGTGCGCGACCCC
TTCGTGCGCCTGATCTCCGCCTTCCGCGAGCAAGTTCGAGCTGGAGAACGAGGAGTTCACCG
CAAGTTCCCGGTGCCCATGCTGCGGCTGTACGCCAACCACACCAGCCTGCCCGCTCGGCGC
GCGAGGCCTTCCGCGCTGGCCTCAAGGTGTCTTCGCCAACTTCATCCAGTACCTGCTGGAC
CCGCACACGGAGAAGCTGGCGCCCTTCAACGAGCACTGGCGGCAGGTGTACCGCCTCTGCCA
CCCGTGCCAGATCGACTACGACTTCGTGGGGAAGCTGGAGACTCTGGACGAGGACGCGCGC
AGCTGCTGCAGCTACTCCAGGTGGACCGGCAGCTCCGCTTCCCCCGAGCTACCGGAACAGG
ACCGCCAGCAGCTGGGAGGAGGACTGGTTCGCCAAGATCCCCCTGGCCTGGAGGCAGCAGCT
GTATAAACTCTACGAGGCCGACTTTGTTCTCTTCGGCTACCCCAAGCCCGAAAACCTCCTCC
GAGACTGAAGCTTTCGCGTTGCTTTTCTCGCGTGCTGGAACTTGACGCACGCGCACTCC
AGTTTTTTTTATGACCTACGATTTTGCAATCTGGGCTTCTGTGTTCACTCCACTGCCTCTATCC
ATTGAGTACTGTATCGATATTGTTTTTTAAGATTAATATAATTCAGGTATTTAATACGA

1000
900
800
700
600
500
400
300
200
100
0

FIGURE 194

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56112
<subunit 1 of 1, 414 aa, 1 stop
<MW: 48414, pI: 9.54, NX(S/T): 4
MTKARLFRLWLVLGVSVMILLIIVYWDSAGAAHFYLHTSFSPHTGPPLPTPGPDRDRELT
DSDVDEFLDKFLSAGVKQSDLPKETEQQPPAPGSMEE SVRGYDWSPRDARRSPDQGRQQAER
RSVLRGFCANSSLAPPTKERAFDDIPNSELSHLIVDDRHGAIYCYVPKVACTNWKRVMI VLS
GSLLRHGAPYRDPLRIPREHVHNASAHLT FNKFWRRYGKLSRHLMKVKLKKYTKFLFVRDPF
VRLISAFRSKFELENEEFYRKFAVPMRLRYANHTSLPASAREAFRAGLKVSFANFIQYLLDP
HTEKLAPFNEHWRQVYRLCHPCQIDYDFVGKLETLDDEAAQLQLQLQVDRQLRFPPSYRNRT
ASSWEEDWFAKIPLAWRQQLYKLYEADFVLFGYPKPENLLRD

Important features:

Signal peptide:

amino acids 1-31

N-glycosylation sites.

amino acids 134-137, 209-212, 280-283 and 370-373

TNFR/NGFR family cysteine-rich region protein

amino acids 329-332

FIGURE 195

TCGGGCCAGAAATTCGGCACGAGGCGGCACGAGGGCGACGGCCTCACGGGGCTTTGGAGGTGA
AAGAGGCCCAGAGTAGAGAGAGAGAGACCGACGTACACGGGATGGCTACGGGAACGCGCT
ATGCCGGGAAGGTGGTGGTCTGTGACCGGGGGCGGGCGGGCATCGAGCTGGGATCGTGCGC
GCCTTCGTGAACAGCGGGGCCGAGTGGTTATCTGCGACAAGGATGAGTCTGGGGGCCGGGC
CCTGGAGCAGGAGCTCCCTGGAGCTGTCTTTATCCTCTGTGATGTGACTCAGGAAGATGATG
TGAAGACCCTGGTTTCTGAGACCATCCGCCGATTGGCCGCTGGATTGTGTGTCAACAAC
GCTGGCCACCAACCAACCCACACAGAGGCTGAGGAGACCTCTGCCCAGGGATTCCGCCAGCT
GCTGGAGCTGAACCTACTGGGGACGTACACCTTGACCAAGCTCGCCCTCCCCTACCTGCGGA
AGAGTCAAGGGAATGTCATCAACATCTCCAGCCTGGTGGGGGCAATCGGCCAGGCCCAGGCA
GTTCCCTATGTGGCCACCAAGGGGGCAGTAACAGCCATGACCAAAGCTTTGGCCCTGGATGA
AAGTCCATATGGTGTCCGAGTCAACTGTATCTCCCCAGGAAACATCTGGACCCCGCTGTGGG
AGGAGCTGGCAGCCTTAATGCCAGACCCTAGGGCCACAATCCGAGAGGGCATGCTGGCCCAG
CCACTGGGCCGCATGGGCCAGCCCGCTGAGGTGCGGGCTGCGGCAGTGTTCCTGGCCTCCGA
AGCCAACCTTCGACCGGGCATTGAACTGCTCGTGACGGGGGTGACAGCTGGGGTACGGGT
GCAAGGCCAGTCGGAGCAACCCCGTGGACGCCCCGATATCCCTTCCCTGATTCTCTCATTT
CTACTTGGGGCCCCCTTCTTAGGACTCTCCACCCCAAACTCCAACCTGTATCAGATGCAGC
CCCCAAGCCCTTAGACTCTAAGCCAGTTAGCAAGGTGCCGGGTCAACCTGCAGGTTCCCAT
AAAAACGATTTCAGCC

FIGURE 196

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56045

<subunit 1 of 1, 270 aa, 1 stop

<MW: 28317, pI: 6.00, NX(S/T): 1

MATGTRYAGKVVVVTTGGGRGIGAGIVRAFVNSGARVVICDKDESGGRALEQELPGAVFILCD
VTQEDDVKTLVSETIRRFGRLCDVNNAGHHPPQRPETSAQGFRLLELNLGTYTLTKL
ALPYLRKSQGNVINISSLVGAIGQAQAVPYVATKGAVTAMTKALALDESPYGVVNCISPGN
IWTPLWEELAALMPDPRATIREGMLAQPLGRMGQPAEVGAAAVFLASEANFCTGIELLVTTG
AELGYGCKASRSTFPVDAPDIPS

Important features:

N-glycosylation site.

amino acids 138-141

Short-chain alcohol dehydrogenase family protein

amino acids 10-22, 81-91, 134-171 and 176-185

[illegible][illegible]

FIGURE 198

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59294

<subunit 1 of 1, 180 aa, 1 stop

<MW: 20437, pI: 9.58, NX(S/T): 1

MDWPHNLLFLLTISIFLGLGQPRSPKSKRKGGQGRPGPLAPGPHQVPLDLVSRMKPYARMEEY
ERNIEEMVAQLRNSSELAQRKCEVNLQLWMSNKRSLSPWGYSINHDPRIIPVDLPEARCLCL
GCVNFFTMQEDRSMVSVPVFSQVPVRRRLCPPPPRTGPCRQRAVMETIAVGCTCIF

Important features:

Signal peptide:

amino acids 1-20

N-glycosylation site.

amino acids 75-78

Homologous region to IL-17

amino acids 96-180.

FIGURE 199

GCGCGCCAGGCGTAGGCGGGGTGGCCCTTGCCTCTCCCGCTTCTTGA AAAAACCCGGCGGG
CGAGCGAGGCTGCGGGCCGGCCGCTGCCCTTCCCCACACTCCCCGCCGAGAAGCCTCGCTCG
GCGCCCAACATGGCGGGTGGGCGCTGCGGCCCGCAGCTAACGGCGCTCTCGGCCCTGGAT
CGCGGCTGTGGCGCGACGCCAGGCCCCGAGGAGGCCGCGCTGCCGCCGAGCAGAGCCGGG
TCCAGCCCATGACCGCCTCCAACCTGGACGCTGGTGTATGGAGGGCGATGGATGCTGAAATTT
TACGCCCCATGGTGTCCATCTTGCAGCAGACTGATTCAGAATGGGAGGCTTTTGCAAAGAA
TGGTGAATACCTTCAGATCAGTGTGGGGAAGGTAGATGTCAATTCAGAAACAGGTTTGTAGTG
GCCGCTTCTTTGTACCACCTCTCCAGCATTTTTTCATGCAAGGATGGGATATTCCGCCGT
TATCGTGGCCAGGAATCTTCGAAGACCTGCAGAATTATATCTTAGAGAAGAAATGGCAATC
AGTCGAGCCTCTGACTGGCTGGAATCCCCAGCTTCTCTAACGATGTCTGGAATGGCTGGTC
TTTTTAGCATCTCTGGCAAGATATGGCATCTTCACAACATTTTCACAGTGACTCTTGGAAAT
CCTGCTTGGTGTCTTATGTGTTTTTCGTATAGCCACCTTGGTTTTTGGCCTTTTATGGG
TCTGGTCTTGGTGGTAATATCAGAATGTTTCTATGTGCCACTTCCAAGGCATTTATCTGAGC
GTTCTGAGCAGAATCGGAGATCAGAGGAGGCTCATAGAGCTGAACAGTTGCAGGATCGCGAG
GAGGAAAAGATGATTCAAATGAAGAAGAAAACAAAGACAGCCTTGTAGATGATGAAGAAGA
GAAAGAAGATCTTGGCGATGAGGATGAAGCAGAGGAAGAAGAGGAGGAGGACAACTTGGCTG
CTGGTGTGGATGAGGAGAGAAGTGAGGCCAATGATCAGGGGCCCCCAGGAGAGGACGGTGTG
ACCCGGGAGGAAGTAGAGCCTGAGGAGGCTGAAGAAGGCATCTGTAGCAACCTTGCCACG
TGACACAGAGGTGGTGAAGACTCCTTGAGGCAGCGTAAAAGTCAGCATGTCTGACAAAGGAC
TGTAGATTTAATGATGCGTTTTCAAGAATACACACCAAAAACAATATGTGCAGCTTCCCTTTGG
CCTGCAGTTTGTACCAAACTCTTAATTTTTCTCGAATGAGCAAGCTTCTCTTAAAGATGCT
CTCTAGTCATTTGGTCTCATGGCAGTAAGCCTCATGTATATAAGGAGAGTCTTCCAGGTGT
GACAAATCAGGATATAGAAAAACAACCTAGTGTGGGATCTGTTTGGAGACTGGGATGGGAA
CAAGTCTATTTACTTAGGGGTGAGAGAGTCTCGACCAGAGGAGGCCATTCCAGTCCTAATC
AGCACCTTCCAGACAAGGCTGCAGGCCCTGTGAAATGAAGCCAAAGCAGGAGCCTTGGCT
CCTGAGCATCCCCAAAGTGTAACGTAGAAGCCTTGCATCCTTTCTTGTGTAAGATTTTAT
TTTTGTCAAATTGCAGGAAACATCAGGCACCAACAGTGCATGAAAAATCTTTCACAGCTAGAA
ATTGAAAGGGCCTTGGGTATAGAGAGCAGCTCAGAAGTCATCCCAGCCCTCTGAATCTCCTG
TGCTATGTTTTATTTCTACCTTTAATTTTTTCAGCATTTCCACCATTGGGCATTTCAGGCTCT
CCACACTCTTCACTATTATCTCTTGGTCAGAGGACTCCAATAACAGCCAGGTTTACATGAAC
TGTGTTTTGTTCATTTGACCTAAGGGGTTTAGATAATCAGTAACCAATAACCCCTGAAGCTGT
GACTGCCAAACATCTCAAATGAAATGTTGTGGCCATCAGAGACTCAAAAGGAAGTAAGGATT
TTACAAGACAGATTAAAAAAAATTTGTTTTGTGCCAAAATATAGTGTGTTGATTTTTTTTT
AAGTTTTCTAAGCAATATTTTTCAAGCCAGAAGTCTCTAAGTCTTGCCAGTACAAGGTAGT
CTTGTGAAGAAAGTTGAATACTGTTTTGTTTTCATCTCAAGGGGTTCCCTGGGTCTTGAAC
TACTTTAATAATACTAAAAAAACACTTCTGATTTTCTCTCAGTGATGTGCTTTTGGTGAAA
GAATTAAGAACTCCAGTACTGAAAGTGAAGATTTGATTTGTTTCCATCTTCTGTAATC
TTCCAAAGAATTATATCTTTGTAAATCTCTCAATACTCAATCTACTGTAAGTACCAGGGAG
GCTAATTTCTTT

FIGURE 200

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56433

<subunit 1 of 1, 349 aa, 1 stop

<MW: 38952, pI: 4.34, NX(S/T): 1

MAGGRCGPQLTALLAAWIAAATAAGPEEAALPPEQSRVQPMTASNWTLVMEGEWMLKFYAP
WCPCSCQQTDSWEAFKNGEILQISVGKVDVIQEPGLSGRFFVTTLPAFFHAKDGI FRRYRG
PGIFEDLQNYILEKKWQSVEPLTGWKSPASLTMSGMAGLFSISGKIWHLHNYFTVTTLGIPAW
CSYVFFVIATLVFGLFMGLVLVVISSECFYVPLPRHLSERSEQNRRSEEAHRAEQLDAAEEK
DDSNEEENKDSLVDDEEEKEDLGDDEEAEEEEEDNLAAGVDEERSEANDQGPFGEDGVTRE
EVEPEEAEEGISEQPCPADTEVVEDSLRQRKSKHADKGL

Important features:

Signal peptide:

amino acids 1-22

Transmembrane domain:

amino acids 191-211

N-glycosylation site.

amino acids 46-49

Thioredoxin family proteins. (homologous region to disulfide isomerase)

amino acids 56-72

Flavodoxin proteins

amino acids 173-187

FIGURE 201

ATCTGGTTGAAC TACTTAAGCTTAATTTGTTAAACTCCGGTAAGTACCTAGCCACATGATT
TGACTCAGAGATTCCTTTTGGTCCACAGACAGTCATCTCAGGGGCAGAAAGAAAAGAGCTCC
CAATGCTATATCTATTACAGGGGCTCTCAAGAACAAATGGAATATCATCCTGATTTTAGAAAAA
TTGGATGAAGATGGATATACTCAATTACACTTCGACTCTCAAAGCAATACCAGGATAGCTGT
TGTTTCAGAGAAAAGGATCGTGTGCTGCATCTCCTTGGCGCTCATTTGCTGTAATTTTGG
GAATCCTATGCTTGGTAATACTGGTGATAGCTGTGGTCCTGGGTACCATGGGGGTCTTTTCC
AGCCCTTGCTCTCTAAATGGATTATATATAGAAAGAGCTGTTATCTATTGAGCATGTCACT
AAATCTCTGGGATGGAAGTAAAGACAATGCTGGCAACTGGGCTCTAATCTCCTAAAGATAG
ACAGCTCAAAATGAATTGGGATTTATAGTAAAAAGTGTCTTCCCAACCTGATAATTCATTT
TGGATAGGCCCTTTCTCGGCCCCAGACTGAGGTACCATGGCTCTGGGAGGATGGATCAACATT
CTCTTTAACTTATTTTCAGATCAGAACCCAGCTACCCAAGAAAACCCATCTCCAAATTGTG
TATGGATTACCGTGTCACTCATTTATGACCAACTGTGTAGTGTGCCCTCATATAGTATTTGT
GAGAAGAAAGTTTTCAATGTAAAGAGGAAGGTTGAGAAAGGAGAGAGAAATATGTGAGGTAGTA
AGGAGGACAGAAAAACAGAAACAGAAAGAGTAAACAGCTGAGGTCAAGATAAATGCGCAAAATG
TTTTAGAGAGCTTGCCCAACTGTAATCTTAACCAAGAAATGAAGGGAGAGGCTGTGATTTCT
GTATTTGTCGACCTACAGGTAGGCTAGTATTATTTTCTAGTTAGTAGATCCCTAGACATGG
AATCAGGGCAGCCAAAGCTTGAGTTTTATTTTTTATTTATTTATTTTTTGAGATAGGGTCT
CACTTTTGTACCCAGGCTGGAGTGCAGTGGCACAATCTCGACTCACTGCACTATCTCTCGC
CTCAGCCCTCAAGTAGCTGGGACTACAGGTGCATGCCACCATGCCAGGCTAAATTTTTGGTG
TTTTTTGTAGAGACTGGGTTTTTGGCCATGTTGACCAAGCTGGTCTCTAAGCTCTGGGCTTAAAG
TGATCTGCCCGCTTGCCCTCCCAAAGTGTCTGGGATTACAGATGTGAGCCACCCACACCTGGC
CCCAAGCTTGAATTTTCAATCTGCCCATTGACTTGGCATTTACCTTGGGTAAAGCCATAAGCGA
ATCTTAATTTCTGGCTCTATCAGAGTTGTTTCATGCTCAACAATGCCATTGAAGTGACACGGT
GTGTTGCCACGATTTGACCCCTCAACTTCTAGCAGTATATCAGTTATGAACTGAGGGTGAAAT
ATATTTCTGAATAGCTAAATGAAGAAATGGGAAAAAATCTTCACCACAGTCAGAGCAATTTT
ATTATTTTTCATCAGTATGATCATAATTTATGATTATCATCTTAGTAAAAAGCAGGAACTCCTA
CTTTTTCTTTATCAATTAATAGCTCAGAGAGTACATCTGCCATATCTCTAATAGAATCTTT
TTTTTTTTTTTTTTTTTTTGGACAGAGTTTCGCTCTTGTGCCCAGGCTGGAGTGCAACGG
CAGGATCTCGGCTCACCGCAACCTCCGCCCCCTGGGTTCAAGCAATTCCTCTGCCTCAGCCT
CCCAAGTAGCTGGGATTACAGTCAGGCACCCACACCCGGCTAAATTTTGATTTTTTTTAGT
AGAGACAGGGTTTTCCATGTCCGTCAGGGTAGTCCCGAACTCTGACCTCAAGTGATCTGC
CTGCCTCGGCCCTCCCAAGTGTCTGGGATTACAGGCGTGAGCCATGCAACCCAGCCTAGAACTCT
TGTATAATATGTAATTTAGGGAAACTGCTCTCATAGGAAAGTTTTCTGCTTTTTTAAATACA
AAAAATACATAAAAAATACATAAAATCTGATGATGAATATAAAAAAGTAAACCAACCTCATTGGA
ACAGATTTAAACATTTTGGAAATATGTTTTATTAGTTTTGTGATGTACTGTTTTACAATTTTT
ACCATTTTTTTTTCAGTAAATTTACTGTAAAAATGGTATTATTGGAATGAAACTATATTTTCCCTATG
TGCTGATTTGTCTTATTTTTTTCATACTTTCCCACTGGTGCTATTTTTATTTCCAATGGATA
TTTCTGATTACTAGGGAGGCATTACAGTCTCTAATGTTGATTAAATATGTGAAAAGAAAT
TGTACCAATTTTACTAAATTATGCAGTTTAAAAATGGATGATTTTATGTTATGTGGGATTCAT
TTCATTAATAAAAAAACTCTTATCAAAAAAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 202

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53912

<subunit 1 of 1, 201 aa, 1 stop

<MW: 22563, pI: 4.87, NX(S/T): 1

MEYHPDLENLDEDGYTQLHFDSQSNTRIAVVSEKGSAAAPPWRLIAVILGILCLVILVIAV
VLGTMGVLSSPCPPNWIIYEKSCYLFSMSLNSWDGSKRQCWLGSNLLKIDSSNELGFIVKQ
VSSQPDNSFWIGLSRPQTEVPWLWEDGSTFSSNLFQIRTTATQENPSPCNVWIHVSVIYDQL
CSVPSYSICEKKFSM

Important features:

Type II transmembrane domain:

amino acids 45-65

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 197-200

N-myristoylation sites.

amino acids 35-40 and 151-156

Homologous region to LDL receptor

amino acids 34-67 and 70-200.

FIGURE 203

GGAAGGGGAGGAGCAGGCCACACAGGCACAGGCCGGTGAGGGACCTGCCAGACCTGGAGGGCTCTCGCTCTGTCA
 CACAGGCTGGAGTGCAGTGGTGTGATCTTGGCTCATGTAACCTCCACTCCCGGGTTCAGAGTATTCTCATGGCC
 TCAGCTCCCGAGTAGCTGGGATTACAGGTGGTGACTTCCAAGAGTGAAGTCCGTGGAGGAAATAGTCTCCCGAG
 TGGCTGTCTGCAGACGACACTGTTCTCTGTCTGAGTCTGCTCTTCTGGTCCAAGAGTGCCACGGCAGGGCCACAGG
 GAAGACTTTCGCTTCTGCAGCCAGCGGAACAGACACACAGGAGCAGCTCCACTACAAACCCACACCCAGAGACTG
 CGCATCTCCATCGAGAACTCCGAAGAGGCCCTCACAGTCCATGCCCTTCCCTGCAGGCCACCCCTGCTCCGGA
 TCCTTCCCTGACCCAGGGGCTCTACCACTTCTGCCTTACTGGAACGACATGCTGGGAGATTACATCTTCTC
 TATGGCAAGCTGACTTCTTGTCTGAGTGACAAAGCTCTAGCTCTCTGCTTCCAGACACAGGAGGAGAGCCTG
 GCTCAGGGGCCCCCGCTGTAGCCACTTCTGTCACTCTGGTGGAGCCCTCAGAACATCAGGCTGCCAGTGGCC
 GCGAGCTTCACTTCTCTTCCACAGTCTCTCCCAACAGCGCCCTCACAATGCTCTGGTGGAGATGTGGAGCTC
 AAAAGGGGACTCCAGCTGCTCAGCCAGTCTCTGAGAGTATCCCGAGAAGGCCCTCAAGGAGGCCCTCGGCTGCCGCC
 GCCAGCCAGCAGTGTGCAGAGCCTGGAGTCGAAACTGACCTCTGTGAGATTATGGGGGACATGGTGTCTCTCGAG
 GAGGACCGGATCAAGCCACAGTGTGGAAGCTCCAGGCCACAGCGGCCCTCCAGGACCTGCACATCACTCCCGG
 CAGGAGGAGGAGCAGAGCCAGATCATGGAGTACTCGGTGCTGCTGCTCGAACACTCTTCCAGGAGCAGAAAGGC
 CGGAGCGGGGAGGCTGAGAAGAGACTCTCTCTGTGGACTTACGAGCAGCCAGCCCTGTTCCAGGACAGAAATCC
 AGCCAAGTCTCGGTGAGAAGGTCTGGGGATTGTGGTACAGAACACAAAGTAGCCAACTCACAGGAGCCCGTG
 GTGCTCACTTCCAGCACCAGTACAGCCGAAGAATGTGACTCTCAATGTGTGTGTGGTGTGAAGACCCCA
 TTGAGCAGCCCGGGCATTTGGAGCAGTCTGGGTGTGAGACCGTCAGGAGAGTAACCCGAACTCTGCTCTGTG
 AACCACTTGACTACTTTGACGTCTGATGGTCTCTCGTGGAGGAGTGGACCGCTGCACAGACTCTCTGAGC
 TACTCTCTCTGCTGTGCTGTGTCTGTCTGTCCCTGGCTGCTGTGACCTTGTACCTTCCCTTCTCTCGAG
 GTGCCCTCGCTGTGAGGAGAAACCTCGGGACTACACCATCAAGGTGCATGAACACTCTGCTGCTGCTCTTCT
 CTGCTGGCAGCAGAGTCTCTCTGTGCGAGCCGCTGGGCTGTGAGGCTGTGAGGCTGTGCTGCGAGCAGTGC
 ATGCTCTGCTACTTCTCTCTGCTCACTCTGCTCTTCTGGATGGGCTCGAGGGGTACAACTCTACCGACTCTGT
 GTGAGGTCTTTGGCAGCTATGCTCTGGCTACTACTCAAGCTGAGCGCACTGGGCTGGGCTCTCCACTCTT
 GTGTCAGCTGGTGGCTCTGTGGATGGGAACTATGGCCCATCATCTTGGCTGTGCATGAGACTCCAGAG
 GCGGTCTACTCTACCTTCCACTTGGTGTGGATCGGGACTCCCTGGTCACTACATCAACCACTCGGCTCTTCTGAGC
 CTGGTGTCTTCTGTTCAACATGGCCATGTAGCCACCATGTTGGTGCAGATCTCGCGCTGCGCCCCACACCCAA
 AAGTGGTCACATGTGTGACACTCTGGGCTCAGCTGCTGTGAGCTGTGCTGTGCTGCTGCTGGGCTTGAATCTCTCTCTC
 TTTGCTTCTGACACTCTCCAGCTTGTCTCTCTACTACTTTCAGCATCACTCACTCTTCCAGGGTCTCTCATC
 TTACTCTGTACTGTGCTGATCGGCTGAGGAGTGGGCGGTTGCCATGGTGGACGAGTCCCGGCTGGGCTTTGAATGT
 GCTTGGGAGTACTCTGGCTCTCACTCAGCTCCACCGGACTCAGAAAGTGGCGCGGCAATGCTGCTCAGGTAAGT
 TCCCCACATCTCTGCCAAACCCAGCTGGAGGCTGGTCTCTCTTACAAACCCCTGGGCGCCAGCTCATTTGCTGGG
 GGCCAGGCTTGGATCTTGGAGCTCTGGCACATCTTAATCCTGTGCCCTGTCTGGGACAGAAATGTGGCTCCA
 GTTGCTCTGTCTCTGTGGTCACTCTGAGGCACTCTGCATCTCTGTCTTAACTCAGGTGGCACCCAGG
 CGAATGGGGCCAGGCGAGACTCTCAGGGCCAGAGCCTTGGCGGAGGAGGCGCTTGGCAGGAGCACAGCAGC
 AGTCTGCTACTCTGAGGCCAGGCCCTCTCTCTCTGCTCACAGCTGGGGGTCCCCGATCCAAATGCTGTGTTTGGGGA
 GTGGTTTCTCCAGGACTGCTGCTGTGTCTGTGCTGTAATGTGTTGCTACTGCACAGCTCGGCTGCCCCGTGAGCCA
 GGCTCGGTACGATGTGTGGTGGCTGGCTAGGTCCTCTGTCCATCTGGGCTTGTATGAGCTGCATTGCCCCCTG
 CTCACTCTGCAAGACACAGCTCTCAGAGGGCCCTCAGCTCTCTCTGAGGCTCTTGTGTGGCAAGACTGTGGA
 CCATGCCAGTCCGCTGTGTTTTCATCCCACTCCAAGGACTGAGACTGACCTCTCTGTGTGACACTGGCCTA
 GAGCTCTGACACTCTCTAAGAGTGTCTCTCAAGCCCCCAAAATGCTCAGGGCCCTCGGCGGCCATCATGGT
 TAATTTGTGTCCAAACAACACACAGGGTAGATTGTGCGCTTGTGTAGGTGTGAGGACAGATGACCGAAGCTG
 CTCACTCTCTCTGCCAACATCTCAGTCTGTGTATGTGAGGCGTGTGGAAGCAAGAACTCTGGAGCTACAGGGACA
 GGGAGCCATCTTCTGCTGGGAATCTGGAAGACTTCTCGAGGAGTCAAGCTTCAATCTTGACCTTTGAAGAT
 GGGAGGAGTGTCTTTTACGTACCAATCTTTGTGTCTTTTATATTAAGAAAGTACATGTTCTATTTAGAGA
 ATTTGGAACCTGAGAGAGAACTCAAGAGAAATAAAATCAAGCTGTTGTATTCGCTAGCAAAAAA
 AA

100
 200
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 400
 500
 600
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 8600
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 9100
 9200
 9300
 9400
 9500
 9600
 9700
 9800
 9900
 10000

FIGURE 204

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50921
<subunit 1 of 1, 693 aa, 1 stop
<MW: 77738, pI: 8.87, NX(S/T): 7
MTPQSLQLQTTLFLLSLLFLVQGAHGRGHREDFRFCSSQRNQTHRSSLHYKPTDLRISIENSE
EALTVHAPFFPAAHPASRSFPDPRGLYHFCLYWNRHAGRLHLLYGKRDFLLSDKASSLLCFQH
QEESLAQGGPLLATSVTSSWWSPQNISSLPSAASFTFSFHSPPHTAAHNASVDMCELKRDQLLL
SQFLKHPQKASRRPSAAPASQQQLQSLESKLTSVRFMGDMVSFEEDRINATVWKLQPTAGLQD
LHIHSRQEEEQSEIMEYSVLLPRTLFRQTKGRSGEAEKRLLLVDFSSQALFQDKNSSQVLGE
KVLGIVVQNTKVANLTPEPVVLTFFQHQLQPKNVTLCQVFWVEDPTLSSPGHWSSAGCETVRRE
TQTSCFCNHLTYFAVLMSVSEVDVAHKKHLSLLSYVGCVVVSALACLVITIAAYLCSRVP LPC
RRKPRDYTIKVHMNLLLA VFLLDTSFLLSEPVALTGSEAGCRASAI FLHFSLLTCLSWMGLE
GYNLYRLVVEVFGTYVPGYLLKLSAMGWGFPIFLVTLVALVDVDNYGPIILAVHRTPEGVIY
PSMCWIRDSLVS YITNLGLFSLVFLFNMA MLATMVVQILRLRPHTQKWSHVLTLLGLSLVLG
LPWALIFFSFASGTFFQLVVLVLYFSIITSFQGFLIFIWYSMRLQARGGPSPLKNSDSARLP
ISSGSTSSSRI

Important features:

Signal peptide:

amino acids 1-25

Putative transmembrane domains:

amino acids 382-398, 402-420, 445-468, 473-491, 519-537, 568-590
and 634-657

Microbodies C-terminal targeting signal.

amino acids 691-693

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 198-201 and 370-373

N-glycosylation sites.

amino acids 39-42, 148-151, 171-174, 234-237, 303-306, 324-327
and 341-344

G-protein coupled receptors family 2 proteins

amino acids 475-504

[illegible]

TGCGCTGGCGCTGCCTTGTGCAACAATGCCGCTTACTCTGCTTCCAGGTTGCCCTGCCTTGCAGA
GGAAANCNTCGGGACTACACNNTCAAGTGCACATGAACCTGCTGCTGGCCGCTCTTCTGCTG
GACACGAGCTTCTGCTCAGCGNAGCCGCTGGCCCTGACAGGCTCTGAAGGCTGGCTGCCGA
GCCAGTGCCATCTTCTGTCACCTTCTCTGCTCACCTGCCTTTCTTGATGGGCCCTCGAGGGG
TACAACCTCTACCGACTCGTGGTGAGGCTTTTGGCACCTATGTCCCTGGCTACCTACTCAA
GCTGAGCGCCATGGGCTGGGGCTTCCCATCTTTCTGGTGACGCTGGTGGCCCTGGTGGATG
TGGACAACATATGGCCCCATCATCTTGGCTGTGCATAGGACTCCAGAGGGCGTCACTACCCCT
TCCATGTGCTGGATCGGGGACTCCCTGGTCAGCTACATCACCAAGCTGGGCCCTCTTACGCTT
GGTGTTCCTGTTCAACATGG

FIGURE 206

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCTGGTTCCAGGTTCCAGGTTTTTGCTTTGA
 TCCTTTTCAAAAACITGGAGACACAGAAGAGGGGCTCTAGGAAAAAGTTTGGATGGGATTATGTGAAAACATCCCT
 GCGATTCTCTGCTGCCAGAGCAGGCTCGGCGCTTCACCCCACTGCAGCGCTCCCTCGGCGTGGTGAAGAGAC
 TCGGGAGTGCCTGCTTCCAAAGTGGCCCGCTGAGTGAGCTCTCACCCAGTCAGCCAAATGAGCGCTCTTCGGGC
 TTCTCCTGTGCATCTTGCCCTGGCCGGCCAGAGACAGGGGACTCAGCGGAATCCAACCTGAGTAGTAAATTC
 AGTTTTCCAGCAACAAGGAACAGAACAGGATACAAGATCCTCAGCATGAGAGAATTTACTGTGTCTACTAATG
 GAGATATTCACAGCCCAAGGTTTTCTCATACTTATCCAAGAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAG
 AGGAAAATGTATGGATACAACCTTACGTTTGATGAAAGATTGGGCTTGAAGACCCAGAAGATGCATATGCAAGT
 ATGATTTTGTAGAAGTTGAGGAACCCAGTGATGGAATATATTAGGGCGCTGGTGTGGTTCTGGTACTGTACAG
 GAAAAACAGATTTCTAAAGGAAATCAAATTAGGATAAGATTGTATCTGATGAATATTTCTCTCTGAAACAGGGT
 TCTGATCCACTACAACATTTGTCATGCCACAATTCACAGAAGCTGTGAGTCCTCAGTGCTACCCCTTCAGGTT
 TGCCACTGGACCTGCTTAATAATGCTATAACTGCCTTTAGTACCTTGAAGACCTTATTCGATATCTTGAACAG
 AGAGATGGCAGTTGGACTTAGAAGATCTATAGGCCAAGTTGGCAACTCTTGGCAAGGCTTTGTTTTGGAA
 GAAAAATCCAGAGTGGTGGATCTGAACCTCTAACAGAGGAGGTAAAGATTATACAGCTGCAACCTCGTAACCTCT
 CAGTGTCATAAGGGGAAGAACTAAAGAGAACCGATACCATTTTCTGGCCAGGTTGTCTCTGGTTAAACGCTGTG
 GTGGGAATCTGCCTGTTGTCTCCCAATTCGAATGAATGTCAATGTGTCCCAAGCAAAGTTACTAAAAAATACC
 ACGAGGTCCTTCAGTTGAGACCAAAGACCGGTGTGAGGGGATGACAAATCACTACCCGACGCTGGCCCTGGAGC
 ACCATGAGGAGTGTGATGTGTGTGTCAGAGGGAGCACAGGAGGATAGCCGCATCACCACAGCAGCTCTTGCCCA
 GAGCTGTGCAGTGCAGTGGCTGATTCTATTAGAGAAGCTATGCGTTATCTCCATCCTTAATCTCAGTTGTTGCT
 TCAAGGACCTTTTCATCTTCAGGATTACAGTGCATTCTGAAGAGGAGACATCAACAGAAATTAGGAGTTGTGCA
 ACAGCTCTTTGAGAGGAGGCCATAAGGACAGGAGAAAAGGCTTCAATCGTGAAGAAAATTAATGTGTGAT
 TAAATAGATCAACCGTAAGTTTCAGAGTTTACCATGTACGTATTCACATAGCTGGGTTCTGTATTTCACTGTTCTT
 GATACGGCTTCAGGTTGCTGTGTCAGTACAGGAAAAAATCTGTGCAAGTGAGCACCTGATTCTGGTGGCTCTTAAC
 CTCAAAAGCTTAGTGTCTGGGCTCAAATCGTATAAATCTGGAATTTTTTTTTTTTGTGTCATATTCACAT
 ATGTAAACAGAACATCTCTATGTACTACAACTGGTTTTTAAAGGAACATATGTCATGAATTAACCTGT
 GTCATCTGATAGGACAGACTGGATTTTTCATATTTCTTATTAATTTCTGCCATTTAGAGAAGAGAACTACA
 TTCATGTTTGAAGAGATAAACCTGAAAGAGAGTGGCTTATCTTCACTTTATCGATAAGTCAGTTATTTG
 TTTCTATGTGATCAATTTTATATTTCTCTTTTGACATTAACCTGTGGCTTTTCTAATCTTGTAAATATATCT
 ATTTTACCAAAGGATATTATATTTCTTTTTATGACAACTTAGATCAACTATTTTATAGCTTGGTAAATTTTTCT
 AAACACAATTTGTTATAGCCAGAGGAACAAGATGATATAAATAATGTTGCTGACACAAAATACATGATTTTCA
 TTCTCGTATGGTCTAGAGTAGATTATCTGCATTTTAAAGAACTGAATTTGATAGAAATTTGTAAGTTGCAAA
 GACTTTTGAATAATTAATATCATCTCTGCATCTCTGTTATTGGAGATGAAATAAAAAGCAACTTTGA
 AAGTAGACATTCAGATCCAGCCATTACTAAGCTATTCTCTTTTGGGAAATCTGAGCTAGCTCAGAAAAACAT
 AAAGCACCTTGAAGAAAGACTTGCAGCTTCTGATAAAGCGTCTGTGCTGTGCGATGAGGACACATCCTATTTA
 TTGTGATGTTGGTTTTTATATCTTAAACTCTGTTCCATACACTTGATATAATACATGATATTTTTATGTACA
 GAAGTAGTCTCTTAAACAGTCTATTATGTACTCTGCAATTTAAAGAAAATCAGTAAAAATTTTTGCTGTG
 AAAATGCTTAATATGTTGCTAGGTTATGTGGTGACTATTTGAATCAAAAATGATTGTAATCATCAATAAAGAA
 ATGTGGCTATTTTGGGGAGAAAATTAATAAAAAAAAAAAAAAAAAAGGTTAGGGATAACAGGGTAAATGGGGCC

FIGURE 207

MSLFLGLLLLLTSALAGRQGTQAESNLSSKQFSSNKEQNGVQDPQHERIITVSTNGSIHSPR
FPHTYPRNTVLVWRLVAVENVMIQLTFDERFGLGLEDPEDDICKYDFVEVEEPSDGTILGRWC
GSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQFTEAVSPSVLPSPSALPLDLL
NNAITAFSTLEDLIRYLEPTEPWGLLEDLRYRTPQLLGAKAFVGRKSRVDNLNLTTEVRLY
SCTPRNFSTSEIRELKRDTIFWPGCLLVKRCGNCACCLHNCNECQVPSKVTKKYHEVLQ
LRPKTGVRGLHKSLDLDVALEHHEEDCVCGRGSGTGG

Signal sequence:

amino acids 1-14

FIGURE 208

CCCATCTCAAGCTGATCTTGGCACCTCTCATGCTCTGCTCTCTTCAACAGACCTCTACATTCCATTTTGGGAAGA
 AGACTAAAAATGGTGTTTCCAAATGTGGACACTGAAGAGACAAATCTTATCTCTTTTAAACATAATCTTAATTTCC
 AAACCTCTTGGGGCTAGATGGTTTCCATAAATCTGCCTCTGATGTCACTCTGGATGTTCACAAAGAACCATGTG
 ATCGTGGACTGCACAGACAAGCATTTGACAGAAATTCCTGGAGGTATTTCCCAAGAACCCAGCAAGCTTACCCCTC
 ACCATTAACACATACCCAGACATCTCCCCAGCGTCTTTACAGACTGGACCATCTGGTAGAGATCGATTTCAGA
 TGCAACTGTGTACCTATTTCACATGGGGTCAAAAAACAACATGTGCACTCAAGAGGCTCGAGATTAAAGCCAGAAAGC
 TTTAGTGGACTCACTATTTTAAATCCCCTTACCTGGATGGAAACAGCTACTAGAGATACCGCAGGGGCTCCCG
 CCTAGCTTACAGCTCTCAGCCTTGAAGCCAAACATCTTTCCATCAGAAAAGAGAATCTAACAGAACTGGGCC
 AACATAGAAATACTCTACCTGGGCGAAAACCTGTTATTATCGAAATCTTGTATTGTTTCATATTCAATAGAGAAA
 GTGCGCTTCTTAACTTGCACAAAGTTAAAAGTGCTCTCCCTGAAAGATAACAATGTGACAGCGTCCCTACTGGT
 TTGCCATCTACTTTAAAGCAACTATATCTCTCAACAACATGATGTGCAAAAATCCAGAAGATGATTTTAAATAAC
 CTCAACCAATTACAAATCTTGACCTAAGTGGAAATTGCCCTCGTTGTTTATAATGCCCATTTCTCTGTGGCGCG
 TGTAAAAAATTTCTCCCTACAGATCCCTGTAATGCTTTTGTGCGCTGACAGAAATTAAGTTTACGCTCA
 CACAGTAACTCTTTCAGCATGTGCCCCAAGATGGTTAAGAACATCAACAACTCAGGAACCTGGATCTGTCC
 CAAAACCTCTTGGCCAAAGAAATTTGGGATGTCTAAATTTCTGCAATTTCTCCCGAGCTCATCCAAATGGATCTG
 TCTTTCAATTTTGAACCTCAGGTCTATCGTGCATCTATGAATCTATCAACAAGCATTTTCTTCACTGAAAAGCGT
 AAAATCTCGCGATCAGAGGATATGTCTTAAAGAGTTGAAAAGCTTTAAACCTCTCGCATTACATAATCTTCAA
 AATCTTGAAGTTCTTGATCTTGGCACTAACTTTATAAAAATGTCAAACCTCAGCATGTTTAAACAATTTAAAGA
 CTGAAAGTCATAGATCTTTTCAGTGAATAAAATATCACTTCAGGAGATTCAAGTGAAGTTGGCTTCTGTCTAAAT
 GCCAGAACTTCTGTAAGAAAGTTATGAACCCAGGCTCTGGAACAATTAACATTATTTTCAGATATGATAAGTATGCA
 AGGAGTTGCAGATTCAAAAACAAGAGGCTTCTTTCATGCTGTTAATGAAAGCTGCTACAAGTATGGGCAGAGC
 TTGGATCTAAGTAAAAATAGTATATTTTGTCAAGTCTCTGATTTTTCAGCATCTTTCTTCTTCTCAAAATGCGCT
 AATCTGTGAGGAATCTCATTAGCCAACTCTTAATGGCAGTGAATTTCAAACCTTTAGCAGAGTCAGATATTTG
 GACTTCTCCAACAACCGGCTTGATTTACTCTCATTCACAGCATTTGCAAGAGCTTCAACAATGGAAGTTCTGGAT
 ATAAGCAGTAATAGCCATTATTTTCAATCAGAAGGAATTAATCATATGCTAACTTTACCAAGAACCTAAAGGTT
 CTGCAGAAACTGATGATGAACGACAAATGACATCTCTCTCCACAGCAGCACTGGAGAGTGAGTCTCTTAGA
 ACTCTGGAATTCAGAGGAAATCATTAGATGTTTATGGAAGAGAGTGATAACAGATACCTTAACAATTTTCAAG
 AATCTGTAAATTAGAGAAATTAGACATCTCTAAAATCCCTAAGTTTCTGCTTCTGGAGTTTTCATGATGTT
 ATGCTCTCAAAATCTAAGAATCTCTCTTGGCCAAAATGGGCTCAAACTCTTTCAGTGGAGAAACCTCCAGTGT
 CTAAGAAGACCTGGAACCTTTGGACCTCAGCCACAAACCTGACCATGCTCTCTGAGAGATTTCAACCTGTCTCC
 AGAAGCTCAAGATCTGATCTTCTAAGAATAATCAAAATCAGGAGCTGACGAAGATTTTCTCAAGATGCGCTC
 CAGTTGCGATATCTGATCTCAGCTCAAAATAAATCCAGATGATCCTCAAGAGACCGACTTCCAGAAAATGTCCTC
 AACAACTCTGAAGATGTTGCTTTTGCATCAATAATCGGTTTCTGTGCACTGTGATGCTGTGGTTTCTGTGGTGG
 GTTAAACATACGAGAGTGACTATCTTACCTGCGCCACAGATGTGACTTGTGGGGGCGAGAGCACAAAGGGC
 CAAAGTGTGATCTCCCTGATCTGTACACCTGTGAGTTAGATCTGACTAACCCTGATTCTGTTCTCACTTTCCATA
 TCTGTATATCTCTTTCTCATGTGTGATGATGACAGCAAGTCACCTCTATTCTGGGATGTGGGTATATTACCATT
 TTCTGTAAAGCAAGATAAAGGGATATCAGCGTCTAATATCACAGACTGTGCTATGATGCTTTTGTGTTAT
 GACATCAAGAACCCAGCTGTGACCGAGTGGGTTTGTGCTGAGCTGGTGGCCAACTGGAAGACCCAGAGAGAAA
 CATTTTAAATTTATGCTCAGGAGAAAGGACTGGTTACCAAGGCGAGCAAGCTTTCCAGCAAGTATTTAC
 TGTGCCATCAGAGGCTCATGGATGAAAAAGTTGATGTGATTTCTGATATTTCTGAGAAGCCCTTTCAGAAG
 TCCAGTCTCTCAGCTCGGAAAAAGGCTCTGTGGAGTCTGTGCTTGTGAGTGGCCAAACAACCCGCAAGCTCAC
 CCAATCTCTTGGCAGTGTCTAAGAGAGCCCTGGCCACAGACAATCATGTGGCCATATGATCAGGTGTTCAAGGAA
 ACGGCTTAGCCCTTCTTGTCAAAACCAACTGCTCTAATTTTCAAGAGAGGCGCTGGC

10037036-1024704

FIGURE 209

MVFPMWTLKRQILILFNIILISKLLGARWFPKTLPCDVTLDVPKNHVIDCTDKHLTEIPGG
IPTNTNLTITINHIPDISPASFHRLDHLVEIDFRNCNCVPIPLGSKNNMCIKRLQIKPRSFS
GLTYLKSLYLDGNGQLLEIPQGLPPSLQLLSLEANNIFSIKRENLTLANIEILYLGQNCYR
NPCYVSYSIEKDAFLNLTCLKVLSLKDNNVTAVPTVLPSTLTLEYLYNNMIAKIQEDDFNNL
NQLQILDLSGNCPRCYNAPFCAPCKNNSPLQIPVNAFDALTELKVLRLHSNSLQHVPPRWF
KNINKLQELDLSQNFLAKEIGDAKFLHFLPSLIQLDLSFNELQVYRASMNLSQAFSSLSKL
KILIRGYVFKELKSFNLSPLHNLQNLEVLDLGTNFIKIANLSMFKQFKRLKVIDLSVNKIS
PSGDSSEVGFCSNARTSVESYEPQVLEQLHYFRYDKYARSCRFKNKEASFMSVNESCYKYGQ
TLDLSKNSIFFVKSSDFQHLSFLKCLNLSGNLISQTLNGSEFQPLAELRYLDFSNNRLDLLH
STAFEELHKLEVLDISSNSHYFQSEGITHMLNFTKNLKVQLKLMNDNDISSSTSRTMESES
LRTLEFRGNHLDVLWREGDNRYLQLFKNLLKLEELDISKNLSFLPSGVFDGMPPNLKNLSL
AKNGLKSFSWKKLQCLKNLETLDLSHNQLTTVPERLSNCSRSLKNLILKNNQIRSLTKYFLQ
DAFQRLRYLDLSSNKIQMIQKTSFPENVLNNLKMLLLHHNRFCLCTDAVWVFWVNHTVETIP
YLATDVTCVGPAGAHKGQSVISLDLYTCELDLTNLILFSLISISVSLFMMVTASHLYFWDVW
YIYHFCAKIKGYQRLISPCCYDAFIVYDTKDPVTEWVLAEVLAKLEDPREKHFNLCLEE
RDWLPGQPVLENLSQSIQLSKKTVFVMTDKYAKTENFKIAFYLSHQRLMDEKVDVILIFLE
KPFQKSKFLQLRKRLCGSSVLEWPTNPQAHYPYFQCCLKNALATDNHVAYSQVFKETV

Signal sequence:

amino acids 1-26

Transmembrane domain:

amino acids 840-860

FIGURE 210

GGGTACCATTCTGCGCTGCTGCAAGTTACGGAATGAAAAATTAGAACCAACAGAAACATGGAAAAATGTTCTCTTC
AGTCGTCAATGCTGACCTGCAATTTTCTGCTAATATCTGGTCTCTCTGAGTTATGCGCGCGAAGAAAAATTTTCTTA
GAAGCTATCCTGTGATGAGAAAAAGCAAATGACTCAGTTATTGCAGAGTGCAGCAATCTGCGACTACAGGAAGT
TTTCCCAAACGGGTGGGCAATATGTGACAGAACTAGACCTGCTGTGATAATTTTATCACACATTAACGAATGAAT
CATTCTCAAGCGTGCAAAATCTCACTAAAATAATCTAAACCAACCCCAATGTACAGCAGCAAGACGGAATCT
CCGGTATACAATCAAAATGGCTTGAATATCAACAGACGGGGCAATCTCAACCTAAAAAACCTTAAGGGAGTTATCTGC
TTGAAGACAAACAGATTACCCCAAATACCCCTCTGGTTGGCCAGAGTCTTTGACAGAACTTAGTCTAATTCAAAAA
ATATATACAACTAACTAAAGAGGGGCATTTCAGAGCTTATAAATCTGAAAACTCTATTTGGCCCTGGAATGCT
ATTTTAAACAAGTTTGCAGAAAACTAACATAGAAGATGGAATATTGAAACCGCTGACAAATTTGGAGTTGCTAT
CACTATCTTTCAATTTCTCTTTACACGTCGCCAACTGCCCAAGCTCCCTACGCAAACTTTTCTGAGCAACA
CCAGATCAATACATATAGTGAAGAAGATTTCAGGGAGTGATAAATTTAACTTACTAGATTTAAGCGGGAAT
GTCCGAGGTGCTTCAATGCCCCATTTCATGCGTGCTTGTGATGGTGGTCTCAATTAATATAGATCGTTTGTG
CTTTTCAAACTTGACCCAACTTCGATACCTAAACCTCTCTAGCACTTCCCTCAGGAAGATTAAATGCTGCCGTGT
TTAAAAATATGCTCATCTGAAGGTGCTGGATCTTGAACTCAACTATTAGTGGGAGAAATAGTCTCTGGGGCAT
TTTAAACGATGCTGCCCGCTTAGAAATACTTGACTGTCTTTAACTATATAAAGGGGAGTTATCCACAGCAT
TTAATATTTCAGAAACTCTCTAAACTTTGTCTCTACGGGCATTCATTTAAAGAGTTATGTGTTCCAGAAC
TCAGAGAAGATGATTTCCAGCCCTGATGCGACTTCCAACTTATGCACTTCAACTTGGGTATTAATTTTATTA
AGCAAATCGATTCTTCAAATTTTCAAATTTCTCCAATCTGAAATATTTATGTGACAGCAACAGAAATACAC
CGTTGTGAAGAATACCCGGCAGAGTTATGCAAAATAGTCTCTCTTTCAACGTCATATCCGGAAACGACGCTCAA
CATTTTGGAGTTTGACCAACTCTGAACTTTTATCACTTTCAACCGTCTTAAATGAAGCCAAATGTGCTGCT
ATGAAAGAGCCTTAGATTAAAGCTCAACAGTATTTTCTTCAATGGGCAACCAATTTGAAATCTTCTCTGACA
TTGCTGTTTAAATCTGTCTGCAAAATAGCAATGCTCAAGTGTAAAGTGAACCTGAATTTGACCACTTCTCTATG
TCAATATTTGGATTGTGACAAACAAATAGACTAGACTTGTATATGCTAGTGTCTTCTGAATTTGTCGACTTGG
AAGTCTAGACTCTCAGCTAATTTTCACTATTTTCAAGATAGCAGCGCTAACACATCATAGAAATTTTCAA
ATTTCAAAATCTAAAGTTTAACTTGAGCCACAACAACATTTATATCTTAAACAGATAAGTATAGACCTGAAA
GCAAGTCCCTGGTAGAATTTTGTTCAGTGGCAATCTGCACTTGCATTTTGTGGAATGATGATGACACAGGTATA
TCTCCATTTCAAAGGTCTCAAGAACTGACACGCTGGAATTTATCCCTTAATAGGCTGAAGCAACATCCCAATG
AAGCATTCCTTAATTTGGCCAGCGAGTCTCACTGAACTACATATAAATGATAATGTGTTAAAGTTTAACTGGA
CATTACTCCAGCAGTTTCTCCCTCTCGAGTTGCTTGACTTACGTGGAAACCAACTCTCTTTTAACTGATAGCC
TATCTGACTTTACATCTCTGCTTCGGACACTGCTGCTGAGTCATACAGGAGTTTCCCACTTACCCCTTGGGCTTC
TTTCTGAGTCACTAGTCTGAAGCACTCGAATTTAAAGTTCCTTCAATCTGCTAAAACCAATCAACAAATTCGCACTT
AAACTAAGACCAACCAAAATTTCTATGTTGGAATACACGGAACCCCTTTGAATGCACTGTCGATTTGGAAG
ATTTCCGAGATGGATGAGTGAACATCTGAAATGCAAAATTCAGAGCTGGAGATGTCAATTTGCGCAAGTCTG
GGCATCAAGAGGAGAGATTTGTGAGTCTGGAGCTAACCACTGTGTTTCAGATGCTGCTGAGTGATATTTAT
TTTTCTCAAGTCTTTATCACCACTAGTTATGTTGGCTGCCCTGGCTCACCAATTTGTTTACTGGGATGTTT
GGTTATATATAATGTGTTTAGCTAAGGTAAGAGGCTACAGGTTCTCTTCCACATCCCAAACTTTCTATGATG
CTACATTTCTTATGACACCAAGATGCTCTGTGTTACTGACTGGGTGATAAATGAGCTGCGCTACCACTTGAAG
AGAGCCGAGCAAAAACGTTCTCTTGTCTAGAGGAGAGGGGATTGGGACCCGGGATTTGGCCATCATCGACAAC
TCATCGAGAGCATCAACCAAGAGCAAGAAAAAGTATTTGTTTAAACCAAAATATGCAAAAAGCTGGAACCTTTA
AAACAGCTTTTACTTGGCTTTGACAGGCTTAATGGATGAGAAATGGAATGTGATTTATTTATCTGCTGGAGC
CAGTGTACAGCATCTCAGTATTTGAGGCTACCGCAGCGGATCTGAAGAGCTCCATCTCCAGTGGCTGACA
ACCCGAGGCAAGAGGCTGTTTGTGGCAACTCTGAGAAATGTGGTCTTGACTGAAATGATTACAGGTATAACA
ATATGATGTGCAATCCATTAAAGCAATACTAACTGACGTTAAGTCATGATTTGCGCGCATAAATAAGATGCAAG
GAATGACATTTCTGATTAGTTATGTTATGCTATGTAACAAATATCCCAAACTTCTGTGGTTTAAAAACAACA
TTTGCTGGCCCAAGTTTGTAGGCTCAGGAGCCAGCATAACTGGGCTTCTGCTCAGGCTGCTCTGACG
AGGCTGCAATGTAGTGTTCACAGAGACATAGGCATCACTGGGCTCACACTGATGTTGTTTGTCTGATGATA
ATTTCTCTGGGCTATGGCCAAAGCTATCACTCATGTAAGCCATGGAGCTCTCCCAAGAGCAGCTGTCTTC
ATCAGAGCTAGCAAAAAGAGAGGTTGTAGCAAGATGAAGTCAACATCTTTGTAATCGAATCAAAAAGATGAT
ATCTCATCACTTTGGCCATATTTCTATTTGTAGAAGTAAACCAAGCTCCCAAGCTCCAGGAGTACGACCA
TCAGTCCAGGGAACACAGCTGAGCAACCAAGATGTTGAGCTCTGATGCTTCACTTGTGCTCACTTATTTCCCT
TGACTGCTGTCTGGGATGGCTGCTATCTTGATGATAGATTGTAATCTAGGAGCAGGATCACTGTGGAC
ATCTTAGCAGTTGACTTAAACATCTCTTTTCAATATCAAGAACTTTTGGCACTGTGACTAATGTGCTTAATA
TTAAGCTTGTGTTTATTTATTTATATATCTATGCTGACATGCTTATATTATGCTGTGGTTCGGTTCGGTTTAT
TTACAGTTGCTTTTAAACAAATTTGCTGTAACATTTGACTTCTAAGTTTGAATGCCATTTAAGAGCTGAGATG
ATAGCTTTTAAAGCATCTTTTACTCTTACCATTTTTAAAGTATGCGAGCTAAATTCGAAGCTTTTGGTCTATA
TTGTTAATTGCCATGTGTAATCTTAAATGAATGAATAAAATGTTTCAATTTTCAAAAAAAAATAAAAA

FIGURE 211

MENMFLQSSMLTCIFLLISGSCELCAEENFSRSYPCEKKQNDSVIAECSNRRLQEVPTVG
KYVTELDLSDNFITHITNESFQGLQNLTKINLNHNPNVQHONGNPGIQSNGLNITDGAFLNL
KNLRELLLEDNQLPQIPSGLPESLTELSLIQNNIYNITKEGISRLINLKNLYLAWNCYFNKV
CEKTNIEDGVFETLTNLELLSLSFNSLSHVPPKLPSSLRKLFSLNTQIKYI SEEDFKGLINL
TLLEDLSGNCPRCFNAPFPCVPCDGGASINIDRFQNLTLQRYNLNSTSLRKINAAWFKNM
PHLKVLDLFENYLVGEIVSGAFLTMLPRLEILDLSFNKIKGSYPQHINISRNFSKLLSLRAL
HLRGYVFQELREDDFQPLMQLPNLSTINLGINFIKQIDFKLFQNFNSNLEIIYLSNENRISPLV
KDTRQSYANSSSFQRHIRKRRTDFFDFPHSNFYHFRPLIKPQCAAYGKALDLSLNSIFFI
GPNQFENLPDIACNLNSANSNAQVLSGTEFSAIPHVKYLDLTNNRLDFDNASALTELSDLEV
LDLSYNSHYFRIAGVTHHLEFIQNFNTNLKVLNLSHNNIYTLTDKYNLESKSLVELVFSGNRL
DILWDDDNRYISIFPKGLKNLTRLDLNLRKHIPNEAFLNLPASLTELHINDNMLKFFNWT
LLQQFPRLELLDLRGKNLFLTDSLSDFTSSLRTLLSHNRISHLP SGFLSEVSSLKHLDL S
SNLLKTINKSALETKTITTKLSMLELHGNNPFECTCDIGDFRRWMDHELVKIPRLVDVICASP
GDQRGKSIVSELELTTCVSDVTAVILFFFTFFITMVMLAALAHFLFYWDVWFIYNVCLAKVK
GYRSLSTSQTFFYDAYISYDTKDASVTDWVINELRHYLEESRDKNVLLCLEERDWDPGLAIID
NMQSINQSKKTIVFVLTKKYAKSWNFKTAFYLALQRLMDENMDVIFILLEPVLQHSQYLRL
RQRICKSSILQWPDNPKAEGLFWQTLRNVVLTENDSRYNMYVDSIKQY

Signal sequence:

amino acids 1-26

Transmembrane domain:

amino acids 826-848

FIGURE 212

CCAGGTCCAACCTGCACCTCGGTTCTATCGATTGAATTCCTCCCGGGGATCCTCTAGAGATCCCT
CGACCTCGACCCACGCGTCCGCCAAGCTGGCCCTGCACGGCTGCAAGGAGGCTCCTGTGGA
CAGGCCAGGCAGGTGGGCCTCAGGAGGTGCCCTCAGGCGGCCAGTGGGCCTGAGGCCCCAGC
AAGGGCTAGGGTCCATCTCCAGTCCCAGGACACAGCAGCGGCCACCATGGCCACGCCTGGGC
TCCAGCAGCATCAGCAGCCCCAGGACCGGGGAGGCACAGGTGGCCCCCACCACCCGGAGGA
GCAGCTCCTGCCCTGTCCGGGGGATGACTGATTCTCTCCGCGAGGCCACCCAGAGGAGAA
GGCCACCCCGCTGGAGGCACAGGCCATGAGGGGCTCTCAGGAGGTGCTGCTGATGTGGCTT
CTGGTGTGGCAGTGGGCGGCACAGAGCACGCCTACCGGCCCGGCCGTAGGGTGTGTGCTGT
CCGGGCTCACGGGGACCTGTCTCCGAGTCGTTCTGTGCAGCGTGTGTACCAGCCCTTCCTCA
CCACCTGCGACGGGCACCGGGCTGCAGCACCTACCGAACCATCTATAGGACCGCCTACCGC
CGCAGCCCTGGGCTGGCCCCCTGCCAGGCCCTCGCTACGCGTGTCTCCCCGGCTGGAAGAGGAC
CAGCGGGCTTCTTGGGCCTGTGGAGCAGCAATATGCCAGCCGCATGCCGGAACGGAGGGA
GCTGTGTCCAGCCTGGCCGCTGCCGCTGCCCTGCAGGATGGCGGGGTGACACTTGCCAGTCA
GATGTGGATGAATGCAGTGTCTAGGAGGGGCGGCTGTCCCAGCGCTGCATCAACACCGCCGG
CAGTTACTGGTGCCAGTGTGGGAGGGGCACAGCCTGTCTGCAGACGGTACACTCTGTGTGC
CCAAGGGAGGGCCCCCAGGGTGGCCCCCAACCCGACAGGAGTGGACAGTGAATGAAGGAA
GAAGTGCAGAGGCTGCAGTCCAGGGTGGACCTGCTGGAGGAGAAGCTGCAGCTGGTGTGGC
CCCCTGCACAGCCTGGCCTCGCAGGCACTGGAGCATGGGCTCCCGGACCCCGGCAGCCTCC
TGGTGCACTCCTTCCAGCAGCTCGGCCGCATCGACTCCCTGAGCGAGCAGATTCCTTCTCTG
GAGGAGCAGCTGGGGTCTGTCTCCTGCAAGAAAGACTCGTGA^{CT}GTGCCAGCGCCCCAGGCTG
GACTGAGCCCTCACCGCCCTGCAGCCCCATGCCCTGCCCAACATGCTGGGGGTCCAG
AAGCCACCTCGGGGTGACTGAGCGGAAGGCCAGGCAGGGCCTTCTCTCTTCTCTCTCCCC
TTCTCGGGAGGCTCCCCAGACCCTGGCATGGGATGGGCTGGGATCTTCTCTGTGAATCCAC
CCCTGGCTACCCCCACCTTGCTACCCCAACGGCATCCCAAGGCCAGGTGGGCCCTCAGCTG
AGGGAAGGTACGAGCTCCCTGTGTGGAGCTGGGACCCATGGCACAGGCCAGGCAGCCGGAG
GCTGGGTGGGGCCTCAGTGGGGGTGCTGCCCTGACCCCCAGCACAAATAAAATGAAACGTGA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGGGCGGCCGCACTCTAGAGT
CGACCTGCAGAAGCTTGGCCGCCATGGCCCACTGTATTATTGACGTTATAATGGTTACAAAT

FIGURE 213

MRGSQEVLLMWLLVLAVGGTEHAYRPGRRVCAVRAHGDPVSESFVQRVYQPFLTTCDGHRAC
STYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAATCQPPCRNGGSCVQPGRCR
CPAGWRGDTQCSDVDECSARRGGCPQRCINTAGSYWCQCWEGHSLSADGTL CVPKGGPPRVA
PNPTGVDSAMKEEVQRLQSRVDLLEEKQLQLVLAPLHSLASQALEHGLPDPGSLLVHSFQQLG
RIDSLSEQISFLEEQLGSCSCKKDS

Signal sequence:

1-19

FIGURE 214

GCCAGGCAGGTGGGCCTCAGGAGGTGCCTCCAGGCGGCCAGTGGGCCTGAGGCCCCAGCAAG
GGCTAGGGTCCATCTCCAGTCCCAGGACACAGCAGCGGCCACCATGGCCACGCCTGGGCTCC
AGCAGCATCAGAGCAGCCCCTGTGGTTGGCAGCAAAGTTTCACTTGGCTGGGCCCGCTGTGA
GGGGCTTCGCGCTACGCCCTGCGGTGTCCGAGGGCTGAGGTCTCCTCATCTTCTCCCTAGC
AGTGGATGAGCAACCCACGGGGGCCCGGGAGGGGAACCTGGCCCCGAGGGAGAGGAACCCC
AAAGCCACATCTGTAGCCAGGATGAGCAGTGTGAATCCAGGCAGCCCCAGGACCGGGGAGG
CACAGGTGGCCCCCACCACCGGAGGAGCAGCTCCTGCCCTGTCCGGGGATGACTGATTC
TCCTCCGCCAGGCCACCAGAGGAGAAGGCCACCCCGCTGGAGGCACAGGCCATGAGGGGC
TCTCAGGAGTGCTGTGATGTGGCTTCTGGTGTGGCAGTGGGCGGCACAGAGCACGCCTA
CCGGCCCCGGCGTAGGGTGTGTGCTGTCCGGGCTCACGGGACCTGTCTCCGAGTCGTTCTG
TGCAGCGTGTGTACCAGCCCTTCTCTACCACCTGCGACGGGCACCGGGCTGCAGCACCTAC
CGAACCATCTATAGGACCGCTTACGCCGCAGCCCTGGGCTGGCCCTGCCAGGCCTCGCTA
CGCGTGCTGCCCCGGCTGGAAGAGGACCAGCGGGCTTCCTGGGGCTGTGGAGCAGCAATAT
GCCAGCCGCCATGCGGGAACGGAGGGAGCTGTGTCCAGCCTGGCCGCTGCCGCTGCCCTGCA
GGATGGCGGGGTGACACTTGCCAGTCAGATGTGGATGAATGCAGTGCTAGGAGGGGCGGCTG
TCCCAGCGCTGCATCAACACCGCCGGCAGTTACTGGTGCCAGTGTGGGAGGGGCACAGCC
TGTCTGCAGACGGTACACTCTGTGTGCCCCAAGGGAGGGCCCCCAGGGTGGCCCCCAACCCG
ACAGGAGTGGACAGTGCAATGAAGGAAGAAGTGACAGGCTGCAGTCCAGGCTGGACCTGCT
GGAGGAGAAGCTGCAGCTGGTGCTGGCCCCACTGCACAGCTGGCCTCGCAGGCACTGGAGC
ATGGGCTCCCGGACCCCGGCAGCCTCCTGGTGCACCTTCCAGCAGCTCGGCCGCATCGAC
TCCCTGAGCGAGCAGATTTCTTCTTGGAGGAGCAGCTGGGGTCTGCTCCTGCAAGAAAGA
CTCGTGACTGCCAGCGCTCCAGGCTGGACTGAGCCCTCACGCCGCTGCAGCCCCATG
CCCCTGCCCAACATGTGGGGGTCCAGAAGCCACCTCGGGGTGACTGAGCGGAAGGCCAGGC
AGGGCCTTCTCTCTTCTCTCTCTCTCTCGGGAGGCTCCCAGACCTGGCATGGGAT
GGGCTGGGATCTTCTCTGTGAATCCACCCCTGGCTACCCCCACCTGGCTACCCCAACGGCA
TCCAAGGCCAGGTGGACCCTCAGCTGAGGAAGGTACGAGCTCCCTGCTGGAGCTGGGAC
CCATGGGCACAGGCCAGGCAGCCCCGAGGCTGGGTGGGGCTCAGTGGGGCTGCTGCCTGAC
CCCCAGCACAATAAAATGAAACGTG

FIGURE 215

MRGSQEVLLMWLLVLAVGGTEHAYRPGRRVCAVRAHGDPVSESFVQRVYQPFLTTCDGHRAC
STYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQPGRCR
CPAGWRGDTQCSDVDECSARRGGCPQRCINTAGSYWCQCWEGHSLSADGTL CVPKGGPPRVA
PNPTGVDSAMKEEVQRLQSRVDLLEEKQLQLVLAPLHSLASQALEHGLPDPGSLLVHSFQQLG
RIDLSEQISFLEEQLGSCSCKKDS

Signal sequence:

1-19

FIGURE 216

CCCACGCGTCCGAAGCTGGCCCTGCACGGCTGCAAGGGAGGCTCCTGTGGACAGGCCAGGCA
GGTGGGCCTCAGGAGGTGCCTCCAGGCGGCCAGTGGGCCTGAGGCCCCAGCAAGGGCTAGGG
TCCATCTCCAGTCCCAGGACACAGCAGCGGCCACCATGGCCACGCCTGGGCTCCAGCAGCAT
CAGCAGCCCCCAGGACCGGGGAGGCACAGGTGGCCCCACCACCCGAGGAGCAGCTCCTGC
CCCTGTCCGGGGGATGACTGATTCTCCTCCGCCAGGCCACCAGAGGAGAAGGCCACCCCGC
CTGGAGGCACAGGCCATGAGGGGCTCTCAGGAGGTGCTGCTGATGTGGCTTCTGGTGTGGC
AGTGGGCGGCACAGAGCAGCCTACCGGCCCGGCCGTAGGGTGTGTGCTGTCCGGGCTCAGC
GGGACCTGTCTCCGAGTCGTTCTGTCAGCGTGTGTACCAGCCCTTCTCACCACCTGCGAC
GGGCACCGGGCCTGCAGCACCTACCGAACCATCTATAGGACCGCCTACCGCCGCAGCCCTGG
GCTGGCCCCCTGCCAGGCCTCGCTACGCGTGTCTGCCCCGGCTGGAAGAGGACCAGCGGGCTTC
CTGGGGCCTGTGGAGCAGCAATATGCCAGCCGCCATGCCGAACGGAGGGAGCTGTGTCCAG
CCTGGCCGCTGCCGCTGCCCTGCAGGATGGCGGGGTGACACTTGCAGTCAGATGTGGATGA
ATGCAGTGTAGGAGGGGCGGCTGTCCCAGCGCTGCGTCAACACCGCCGGCAGTTACTGGT
GCCAGTGTGGGAGGGGCACAGCCTGTCTGCAGACGGTACACTCTGTGTGCCCAAGGGAGGG
CCCCCAGGGTGGCCCCAACCCGACAGGAGTGGACAGTGAATGAAGGAAGAAGTGCAGAG
GCTGCAGTCCAGGGTGGACCTGCTGGAGGAGAAGCTGCAGCTGGTGTGGCCCCACTGCACA
GCCTGGCCTCGCAGGCATGGAGCATGGGCTCCCGGACCCCGGCAGCCTCTGGTGCCTCC
TTCCAGCAGCTCGGCCGATCGACTCCCTGAGCGAGCAGATTTCTTCTTGAGGAGCAGCT
GGGGTCTGCTCCTGCAAGAAAGACTCGTGACTGCCCAGCGCCCCAGGCTGGACTGAGCCCC
TCACGCCGCCCTGCAGCCCCCATGCCCTGCCCAACATGCTGGGGGTCCAGAAGCCACCTCG
GGGTGACTGAGCGGAAGGCCAGGCAGGGCCTTCCTCCTCTTCTCCTCCCCCTTCTCGGGAG
GCTCCCCAGACCTGGCATGGGATGGGCTGGGATCTTCTCTGTGAATCCACCCCTGGCTACC
CCCACCTGGCTACCCCAACGGCATCCCAAGGCCAGGTGGGCCCTCAGCTGAGGGAAGGTAC
GAGTCTCCTGTGTGAGCCTGGGACCCATGGCAGAGCCAGGCAGCCCGGAGGCTGGGTGGGG
CCTCAGTGGGGGCTGCTGCCTGACCCCAGCACAAATAAAAATGAAACGTG

FIGURE 217

MRGSQEVLLMWLLVLAVGGTEHAYRPGRRVCAVRAHGDVSESFVQRVYQPFLLTTCDGHRAC
STYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQPGRCR
CPAGWRGDTQCSDVDECSARRGGCPQRCVNTAGSYWCQCWEGHSLSADGTL CVPKGGPPRVA
PNPTGVDSAMKEEVQRLQSRVDLLEEKQLQLVLAPLHSLASQALEHGLPDPGSLLVHSFQQLG
RIDSLSEQISFLEEQLGSCSCKKDS

Signal sequence:

1-19

1-19
20-39
40-59
60-79
80-99
100-119
120-139
140-159
160-179
180-199
200-219
220-239
240-259
260-279
280-299
300-319
320-339
340-359
360-379
380-399
400-419
420-439
440-459
460-479
480-499
500-519
520-539
540-559
560-579
580-599
600-619
620-639
640-659
660-679
680-699
700-719
720-739
740-759
760-779
780-799
800-819
820-839
840-859
860-879
880-899
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920-939
940-959
960-979
980-999
1000-1019
1020-1039
1040-1059
1060-1079
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3120-3139
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FIGURE 218

GGTTCGCCACAGCTGGTTTAGGGCCCCGACCACTGGGGCCCCCTTGTTCAGGAGGAGACAGCCTCCCGGCCCGGGAG
 GACAAAGTCGCTGCCACCTTTGGCTGCGACGCTGATTCCTCGGACGGTCCGTTTCTCGCGCTCAGCTGCGGGCCG
 AGTTGGGTCTCCGGTGTTCAGGCGGGCTCCCCCTTCTCGGTCTCCCTTCTCCGCTCGGGCGGGTTATCGGGAGG
 AGATTGTCTTCAGGGCTAGCAATTGGACTTTTGATGATGTTTGACCAGCGGCGAGGAATTAGCAGGCAACGCTGAT
 TTCAAAGCTGGGCTCAGCCTCTGTTTCTCTCTCGTGTAATCGCAAAACCCATTTTGGAGCAGGAATTCGAATCA
 TGTCTGTGATGGTGGTGAGAAAGAGGTGACACGGAAATGGGAGAACTCCAGGCAGGAAACACCTTTTGTCTGTG
 ATGGCCCGCTCATGATGGCCCGGCAAAAGGGCATTTTCTACCTGACCCCTTTTCTCATCTCGGGACATGTACAC
 TCTTCTTCGCTTTGAGTGCCTTACCTGGCTGTTTCTGCTGCTCCTGCCATCCCTGTATTTGTGCCATGCTCT
 TCTTTTCTCCATGGCTACACTGTTGAGGACCACTTCAGTGAACCTGGAGTGATTCTCGGGCGCTACCAAGATG
 AAGCAGCTTTCATAGAAATGGAGATAGAAGCTACCAATGGTGGGTGCGGTCGCCAGGGCCACGACACCGCTCGTA
 TCAAGAATTTCCAGATAAAACACAGATTTGTGAACTGAAATACCTGTTACACATGCAAGATCTTCGGGCTCCCC
 GGGCTCCCATGCGAGCATCTGTGACAACTGTGTGGAGCGCTTCGACCATCACTGCCCTGGTGGGGAATTTGTG
 TTGGAAAGAGGAACACCGCTACTTCTACCTCTTCATCCTTTCTCTCTCCCTCCTCACAACTCTATGCTCTCGCCT
 TCAACATCGTCTATGTGGCCCTCAAATCTTTGAAATTTGGCTTCTTGGAGACATTGAAAGAACTCCTGGAACTG
 TTCTAGAAGTCTCATTTGCTCTTTTACACTCTGGTCCGTCGTGGGACTGACTGGATTTCATACTTTCTCTGTGG
 CTCTCAACAGACAAACCAATGAAGACATCAAAGGATCATGGAAGGGAAGAAATCGGTCCAGAAATCCCTACAGCC
 ATGGCAATATTTGAAGAACTGCTGTGAAGTGTCTGTGGCCCTTGCCTCCAGTGTGCTGGATCGAAGGGGTA
 TTTTGGCACTGGAGGAAAGTGAAGTGCAGCTCCAGTACTCAAGAGACCAAGTACAGCCCTCTTGCCACAGAGCC
 CAGCCCCCAGAGCAACCTGAACTCAAATGAGATGCCGGAGGACAGCAGCACTCCCGAAGAGATGCCACCTCCAG
 AGCCCCCAGAGCCACCAAGGAGGCGAGTGAAGCTGAGAAAGTACGCTATCTATGGAAGAGACTTTTGTTTGTGTT
 TATTTTAGGGCTATGAGAGATTTTCAAGTGTGAGAAAGTTAAACCTGAGACAGAGAGCAAGTAACTGCTCCCTTTAACT
 GTTTTCTTTTGTGTTCTTAGTCAACCCAGTTGACACTGGCATTCTTGTGCTGCAAGCTTTTAAATTTTGAAGT
 CAAGGCACTGGCCAGAAAGTGTCACTCACTCTGATAACTGGAATAATGGTCTCTCTGGGCCCTGGCACTGGTCTCT
 CCATGGGCTCAGCAACAGGTGCCCTTGGACCCCTCTCTTCCCTCAGATCCAGCCCTCCCTGCTGTGGGTCACT
 TGGTCTCATTTCTGGGGCTAAAAGTTTGTGAGACTGGCTCAAATCTCCCAAGTCTGCTGCACTGCTGAGTCCAGAG
 GGCAGTACAGAGACCTCTGGCCAGGGATCTTAAGTGGCTTTGGGGTCTTCAGGACTCAAGAGAGAGGAGAG
 TGGGTGAGAAGATTCTCTGGCCACCAAGTGGCCAGTATGCCACAAATCTTTTAGGAATGGGACAGGTACTCT
 TCCACTGTTTGTANN
 CAGGAATGGCAGTAAAGTCTGCACTTTGCTCATTTCTTTCTCAGAGGAAGCCCGAGTGTCACTTAAGC
 ACTATCCCCCTCAGACTCCCTGTGAGGGCTCGAGAGGCCCTGAATGCAAAATGGGAACCAAGGCACAGAGAG
 GCTCTCCTCTCCTCTCCTCTCCCCGATGTACCTCAAAAAAAGAAATGCTAACCACTTTCTCATTAAAGCT
 CGCTGAGTGAGGGAAGGCCAGCACTGTGCTCTCGGGTAACTCACCTTAAGGCTCTGGGCCACCTCTGGCT
 ATGTAACACACATGGGGGCTTCTCCAAGCCCGCTCTTCAGCAGCTTCCACGGCAGAGTCCAGAGCCACTT
 CACCTGGGGGTGGGCTGTGGCCCCAGTCAGCTCTCTCAGGACCTGCTCTATTTCAGGGAAGAGATTATGT
 ATTATATGTGGCTATTTTCTAGAGCACCTGTGTTTCTCTTTTAAAGCCAGGTCTGCTCGGATGACTTAT
 GCGGTGGGGAGTGTAACCGGAACCTTTCTATATTGGAAGGCATTAAACTGTGTCCTAATGCA

FIGURE 219

MSVMVVRKKVTRKWEKLPGRNTFCDDGRVMMARQKGFYLTFLILGTCTLFFAFECRYLAV
QLSPAIPVFAAMLFLFSMATLLRTSFSDPGVIPRALPDEAAFIEMEIEATNGAVPQGQRPPP
RIKNFQINNQIVKLKYCTCKIFRPPRASHCSICDNCVERFDHHCPCWVGNCVGNRYRYFYFYL
FILSLSLTIYVFAFNIVYVALKSLKIGFLETLKETPGTVLEVLCFFTLWSVVGLTGFTTF
LVALNQT TNEDIKGSWTGKNRVQNPYSHGNIVKNCCEVL CGPLPPSVLDRRGILPLEESGSR
PPSTQETSSSLLPQSPAPTEHLNSNEMPEDSSTPEEMPPEPPEPPEPQEAEEAEK

Putative transmembrane domains:

amino acids 36-55 (type II TM), 65-84, 188-208, 229-245

FIGURE 220

AAAACCCCTGTATTTTTTACAATGCAAATAGACAATNANCTGGAGGCTTTTGAATTAGGTAT
 TATAGGGATGGTGGGGTTGATTTTNTTCTGGAGGCCTTTGGCTTTGGACTCTCNCTTCT
 CCCACAGAGCNCTTCGACCATCACTGCCCTGGGTGGGGAATTGTGTTGGAAAGAGGAACTA
 CGCGTANTTCTACCTCTTCATCCTTTNTCTCTCCNCCTCACAATCTATGTCTTCGCCTTCA
 ACATCG

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FIGURE 221

GTGTGTCTTTCAGCAAAACAGTGGATTAAATCTCCTTGCAACAAGCTTGAGAGCAACACAA
TCTATCAGGAAAGAAAGAAAGAAAAAACCAGACCTGACAAAAAGAAGAAAGAAAGAAGA
AAAAAATCATGAAAACCATCCAGCCAAAATGCACAATTCTATCTCTTGGGCAATCTTCAC
GGGGCTGGTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGAGATGCCACCTTCC
CCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACATA
GACAACCGGGTCACCCGGGTGGCTAAACCGCAGCACCATCTCTATGCTGGGAATGA
CAAGTGGTGCTGGATCTCGCGTGGTCTTCTGAGCAACACCCAAACGAGTACAGCATCG
AGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACAAC
CACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCAAAATTTAGAGATTTT
TTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGAC
CAGAGCCTACGGTTACTTGGAGACACATCTCTCCAAAGCGGTTGGCTTTGTGAGTGAAGAC
GAATACTTGGAAATTTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTC
CAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTACCGTGAACATATCCACCATA
TTTCAGAAGCCAAGGGTACAGGTGTCCCGTGGGACAAAAGGGGACATGCAGTGTGAAGCC
TCAGCAGTCCCCTCAGCAGAATTCAGTGGTACAAGGATGACAAAAGACTGATTGAAGGAAA
GAAAGGGGTGAAAGTGGAAAAACAGACCTTCTCTCAAACTCATCTTCTTCAATGTCTCTG
AACATGACTATGGGAACTACACTTGCCTGGCTCCAAACAAGCTGGGCCACCAATGCCAGC
ATCATGCTATTTGGTCCAGGCGCGCTCAGCGAGGTGAGCAACGGCAGCTCGAGGAGGGCAGG
CTGCGTCTGGCTGCTGCTCTTCTGGTCTTGACCTGCTTCTCAATTTTGATGTGAGTGCC
ACTTCCCCACCCGGGAAAGGTGCCGCCACCACCACCAACACACAGCAATGGCAACAC
CGACAGCAACCAATCAGATATATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGA
AATTTGAGGGAGGGGAAACAAAGAATACTTGGGGGGAAAAGAGTTTAAAAAAGAAATTGAA
AATTGCCTTGACAGATATTTAGGTACAATGGAGTTTTCTTTTCCAAACGGGAAGAACACAGC
ACACCCGGCTTGACCCACTGCAAGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGGCAA
GGGCTCAGCCTCTCTGCCACAGAGTGCCCCCAGTGGAACATTCTGGAGCTGGCCATCCCA
AATTCAATCAGTCCATAGAGACGAACAGAATGAGACCTTCCGGCCCAAGCTGGCGCTGCGG
GCACTTTGGTAGACTGTGCCACCACGGCGTGTGTTGTGAAACGTGAAATAAAAAGAGCAAAA
AAAA

FIGURE 222

MKTIQPKMHNISISWAIPTGLAALCLFQGVPVRSRGDATFFKAMDNVTVRQGESATLRCTIDNR
VTRVAWLNRSTILYAGNDKWCLDPRVVLNLSNTQTQYSIEIQNVDDVYDEGPFYTCVQTDNHPK
TSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTVRHRISPKAVGVFVSEDEYL
EIQGITREQSGDYECASANDVAAPVVRVRKVTVNYPPYISEAKGTGVPVGQKGLQCEASAV
PSAEFQVYKDDKRLIEGKGKVVENRFLSKLIFFNVSEHDYGNVYTCVANSKLGHTNASIML
FPGPAWSEVSNKGTSSRAAGCVWLPLLVHLHLLEF

Signal peptide:

amino acids 1-28

Abstract

GAAAAAAATCATGAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTTGGGCAATCTTC
ACGGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTT
CCCCAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTA
TTGACAACCGGGTCACCCGGGTGGCTTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAAT
GACAAGTGGTGCCTGGATCCTCGCGTGGTCTTCTGAGCAACACCCAAACGCAGTACAGCAT
CGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACA
ACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAATTTGTAGAGATT
TCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAG
ACCGAG

FIGURE 224

ATGGCTGGTGACGCGGGGCGGGGACGGGGCCGCGGCCCGGGAGCGGGCCAGCTGCCGGAGCCCTGA
ATCACCGCCTGGCCCGACTCCACCTGAACGTCGCGCTGCAGGAGCTGGGAGCTGGCAGCAACGTTGGGATCCAG
AAGGGGACAAGACAGCTGTTAGGCTCACGCACGAGCTGGAGCTGGTCTTAGCAGGTGGCTCTACTGCTGGCT
GCACCTGCTTCTGGGCTGCCCTTGGCCCTAGGGGTCAGTACCACAGAGACCCTCCACAGCACCTGGCCTTACA
GAGGCGTCGATTGCAGTGGCTGGAAAAATCCTGGAGTCCCTGGAACCGAGGGGTGAGCCCTGTGAGGACTTTTAC
CAGTTCTCTGTGGGGGTGGATTCTGGAGGAACCCCTGCGCCGATGGCGTCTCTCGCTGGAAACCTTCAACAGC
CTCTGGGACCAAAACAGGCCATCTGAAGCACTGCTTGAAAAACACACCTTCAACTCCAGCAGTGAAGCTGAG
CAGAAGACACAGCGCTCTACCTATCTTGCTACAGTGGAGCGCATTTAGGAGCTGGGAGCCAGCCACTGAGA
GACCTCATTGAGAAGATTGGTGGTTGGAACTTACGGGGCCCTGGGACGAGGACAACCTTATGAGAGTGTGGAAG
GCAGTAGCAGGACCTACAGGGCCACCCCATTTCTCACCGTCTACATCAGTGGCGACTCTAAGAGTTCCAAACAGC
AATGTTATCCAGGTGGACAGCTCTGGGCTCTTCTGCGCTCTCGGGATTACTACTTAAACAGAACTGCCAATGAG
AAGTGCTCACTGCTCTATCTGGATTACATGGAGGAACCTGGGATGCTGCTGGGTGGGCGGCCACCTCCACGAGG
GAGCAGATGCAGCAGGTGCTGGAGTTGAGATACAGCTGGCCAAACATACAGTGGCCACGAGGACCAGCGGCGCAG
GAGGAGAAGATCTACACAAGATGAGCATTTCGGAGCTGCAGGCTCTGGCGCCCTCCATGGACTGGCTTGAGTTT
CTGTCTTCTGCTGTCCACATTGGAGTTGAGTGACTCTGAGCCTGTGGTGGTGTATGGGATGGATTATTTGCAG
CAGGTGTGAGAGCTCATCAACCGCACGGAACCAAGCATCTGAACAATTACTGATCTGGAACTGGTGCAAAAG
ACAACCTCAAGCCTGGACCGACGCTTTGAGTCTGCACAAGAGAAGCTCTGGGAGACCTCTATGGCACTAAGAAG
TCCTGTGTGTCGAGGTGGCAGACCTGCATCTCCAACACGATGACGCGCTTGGCTTTGCTTTGGGGTCACTCTTC
GTGAAGGCCACGTTTGAACCGCAAGCAAGAAATTGCAGAGGGGATGATCAGCGAAATCCGGACCGCATTGAG
GAGGCCCTGGGACAGCTGTTTGGATGGATGAGAAGACCCGCGAGGACCAAGGAGAAAGCAGATGCCATCTAT
GATATGATGTTGTTTCCAGACTTTATCCTGGAGCCCAAGAGCTGGATGATGTTTATGACGGGTACGAAATTTCT
GAAGATTTCTTTCCAAAAACATGTTGAATTTGTACAACTTCTCTGCCAAGGTTATGCTGACAGCTCCGCAAG
CCTCCACGCCGAGACCAAGTGGAGCATGACCCCCAGACAGTGAATGCTACTACCTTCCAATGAAGATGAGATC
GTCTTCCCGCTGGCATCTCTGAGGCGCCCTTCTATGCGCCGAACCCCAAGGCCCTGAACTTTCGGTGGCATC
GGTGTGGTCAATGGGCCATGAGTTGACGCTGCTTGTATGACCAAGGGCGCGAGTATGACAAAGAACGGAACCTG
CGGCCCTGGTGGCAGAAATGAGTCCCTGGCAGCCTTTCGGAACCAACGCGCTGCATGGAGGAACAGTACAATCAA
TACCAGGTCAATGGGAGAGGCTCAACGGCGCGCAGACGCTGGGGAGGAACATTACTGACAAACGGGGGCTGAAG
GCTGCCCTCAATGCTTACAAGCATGGCTGAGAAAGCATGGGAGGAGCAGCACTGCCAGCCGTGGGCTCACC
AACCACAGCTCTCTTCTGTTGGGATTTGCCCAGGTGTGGTGTCTGGTCCGCAACACAGAGAGCTCTCACGAGGGG
CTGGTGACCGACCCCAACAGCCCTGCCCGCTTCCGCTGCTGGGCACTCTCTCCAACCTCCCGTGACTCTCTGGCG
CACTTCCGCTGCCCTGTGCGCTCCCCCATGAACCCAGGGCAGCTGTGTGAGGTGTGGTAGACCTGATCAGGGGA
GAAATGGCCAGCTGTACAGAGACCTGGGGCAGCTCTCTGCAAAAGCTGTTTGTCTCTGGGTTGGGAGGAAGCAA
ATGCAAGCTGGCTGGGCTCTAGTCCCTCCCCCAACAGGTGACATGATGACAGACCTCTCTCAATCACCACATTG
TGCTCTGCTTTGGGGGTGCCCCCTTCCCTCCAGCAGAGCCCCACCATCTCACTGTGACATCTTTCGTTGTCACCTT
GCCTGGAAGAGGTCTGGTGGGGAGGCCAGTTCCCATAGGAAGGAGTTCGC

FIGURE 225

MNVALQELGAGSNVGFQKGTRQLLGSRTQLELVLAGASLLLAALLLGCLVALGVQYHRDP
STCLTEACIRVAGKILESIDRGVSPCEDFYQFSCGGWIRRNPLPDGRSRWNTFNSLWDQ
ILKHLENTTFNSSSEAEQKTQRFYLSCLQVERIEELGAQPLRDLEKIGGWNITGPWDQDN
FMEVLKAVAGTYRATPFFTVYISADSKSSNSNVIQVDQSGFLPSRDYVLNRTANEKVL
LDYMEELGMLLGGRPSTREMQQVLELEIQLANITVPQDQRDEEKIYHKMSISELQALAP
SMDWLEFLSFLLSPLELSDSEPVVVGMDYLQQVSELINRTEPSILNNYLIWNLVQKTSSL
DRRFESAQEKLETLTYGTTKSCVPRWQTCISNTDDALGFALGSLFVKATFDRQSKEIAEGMI
SEIRTAEEALGQLVWMDEKTRQAAKEKADAIYDMIGFPDFILEPKELDDVYDGYEISEDSF
FQNMLNLNFSKVMADQLRKPPSRDQWSMTPTVNAYYLPKNEIVFPAGILQAPFYARNH
PKALNFGGIGVVMGHELTHAFDDQGREYDKEGNLRPWQNESLAFRNHTACMEEQYNQYQV
NGERLNGRQTLGENITDNGGLKAAYNAYKAWLRKHGEEQQLPAVGLTNHQLFFVGFAQVWCS
VRTPESSHEGLVTDPHSPARFVLGTLNSRDFLRHFGCPVGSMPNPGQLCEVW

Type II Transmembrane domain:
amino acids 32-57

FIGURE 227

GGCCGAGCGGGGTGCTGCGCGGCGGCCGTGATGGCTGGTGACGGCGGGGCCGGGCAGGGGA
CCGGGGCCGCGGCCCGGGAGCGGGCCAGCTGCCGGGAGCCCTGAATCACCGCCTGGCCCCGAC
TCCACCATGAACGTCGCGCTGCAGGAGCTGGGAGCTGGCAGCAACGTGGGATTCCAGAAGGG
GACAAGACAGCTGTTAGGCTCAGCAGCAGCTGGAGCTGGTCTTAGCAGGTGCCTCTCTAC
TGCTGGCTGCAC TGCTTCTGGGCTGCCTTGTGGCCCTAGGGGTCCAGTACCACAGAGACCCA
TCCCACAGCACCTGCCTTACAGAGGCCTGCATTTCGAGTGGCTGGAAAAATCCTGGAGTCCCT
GGACCGAGGGGTGAGCCCTGTGAGGACTTTTACCAGTTCTCCTGTGGGGGCTGGATTTCGGA
GGAACCCCTGCCCGATGGGCGTTCTCGCTGGAACACCTTCAACAGCCTCTGGGACCAAAC
CAGGCCATACTGAAGCACCTGCTTGA AACACACCTTCAACTCCAGCAGTGAAGCTGAGCA
GAAGACACAGCGCTTCTACCTATCTTGCTACAGGTGGAGCGCATTGAGGAGCTGGGAGCCC
AGCCACTGAGAGACCTCATTGAGAAGATTGGTGGTTGGAACATTACGGGGCCCTGGGACCAG
GACAACTTTATGGAGGTGTTGAAGGCAGTAGCAGGGACCTACAGGGCCACCCATTCTTCAC
CGTCTACATCAGTGCCGACTCTAAGAGTTC AACAGCAATGTTATCCAGGTGGACCAGTCTG
GGCTCTTTCTGCCCTCTCGGGATTACTACTTAAACAGAACTGCCAATGAGAAAGTAAGGAAC
ATCTTCCGAACCCCATCCCTACCCCTGGCTGAGCTGGGCTGATCCCTGTTGACTTTTCCCT
TTGCCAAGGTCAGAGCAGGAAGGTGAGCCTATCCTGTACACCTAGTGAACAACTGCCCT
CCTTCTTTCTTCTTTCTTCTTCTCCCTCCCTCCCTTCTTCCCTTTTCTTCTTCTTCTTCC
TCTTATTCTTCTAGTAGGTTTCATAGACACCTACTGTGTGCCAGGTCCAGTGGGGGAATTCC
GAGATATAAGTTTCCGAGCCATTGCCACAGGAAGCGTTTCAGTGTGATGGGTTTCATGGACCT
AGATAGGCTGATAACAAAGCTCACAAGAGGGTCTGAGGATTTCAGGAGACCTTATGGAGCC
AGCAAAGTCTTCTCTGAAGAGATTGCATTTGAGCCAGGTCTCTGTAG

FIGURE 228

ATGCCTACTACCTTCCAATAAGAATGAGATCGTCTTCCCCGCTGGCATCCTGCAGGCCCC
TTCTATGCCCGCAACCACCCCAAGGCCCTGAACCTCGGTGGCATCGGTGTGGTCATGGGCCA
TGAGTTGACGCATGCCCTTTGATGACCAAGGGCGCGAGTATGACAAAGAAGGGAACCTGCGGC
CCTGGTGGCAGAATGAGTCCCTGGCAGCCTTCCGGAACCACACGGCCTGCATGGAGGAACAG
TACAATCAATACCAGGTCAATGGGGAGAGGCTCAACGGCCGCGACGCTGGGGGAGAACAT
TGCTGACAACGGGGGGCTGAAGGCTGCCCTACAATGCTTACAAAGCATGGCTGAGAAAGCATG
GGGAGGAGCAGCAACTGCCAGCCGTGGGGCTCACCAACCACACAGCTCTTCTTCGTGGGATTT
GCCCAGGTGTGGTGCTCGGTCCGCACACCAGAGAGCTCTCACGAGGGGCTGGTGACCGACCC
CCACAGCCCTGCCCGCTTCCGCGTGCTGGGCACTCTCTCAAACCTCCCGTGACTTCTTGCGGC
ACTTCGGCTGCCCTGTTCGGCTCCCCCATGAACCCAGGGCAGCTGTGTGAGGTGTGGTAGACC
TGGATCAGGGGAGAAATGGCCAGCTGTCAACAGACCTGGGGCAGCTCTCCTGACAAAGCTGT
TTGCTCTTGGGTTGGGAGGAAGCAAATGCAAGCTGGGCTGGGTCTAGTCCCTCCCCCCCCACA
GGTGACATGAGTACAGACCCCTCCTCAATCACCACATTTGTGCCTCTGCTTTGGGGGTGCCCT
GCCTCCAGCAGAGCCCCACCATTCAGTGTGACATCTTTCGGTGTCACCCTGCCTGGAAGAG
GTCTGGTGGGGAGGCCAGTTCCCATAGGAAGAGTCTGCCTCTTCTGTCCCCAGGCTCACT
CAGCCTGGCGGCCATGGGGCTGCCGTGCCTGCCCACTGTGACCCACAGGCCTGGGTGGTG
TACCTCCTGGACTTCTCCCCAGGCTCACTCAGTGCACACTAGGGGTGGAAGTCACTCTGTCT
TGGCTACCCCTCACGGGCTACCCCACTCACCCTGTGCTCCTTGTGCCACTGCTCCAGTG
CTGCTGCTGACCTTCACTGACAGCTCCTAGTGGAGCCCAAGGGCCTCTGAAAGCCTCCTGC
TGCCCACTGTTTCCCTGGGCTGAGAGGGGAAGTGCATATGTGTAGCGGGTACTGGTTCTGT
GTCTTAGGGCACAAGCCTTAGCAAATGATTGATTCTCCCTGGACAAAGCAGGAAAGCAGATA
GAGCAGGGAAGGAAGAACAGAGTTTATTTTACAGAAAAGAGGGTGGGAGGGTGTGGTCT
TGGCCCTTATAGGACC

FIGURE 229

CCCACGCGTCCGAGCCGCCGAGAAATTAGACACACTCCGGACGCGGCCAAAAAGCAACCGAGA
GGAGGGGAGGCCAAAAACCCGAAAAACAAAAAGAGAGAAACACACCCCAACACTGGGGTGG
GGGGAAGAAAGAAAGAAAGAAACCCACCCACCCACCAAAAAAATAAAAAA
AAAAAATAAATCTGTGGCGCGCCGCTGGTTCCCGGGAAGACTGCCAGCACCGGGG
TGGGGGAGTGCAGAGTGAAAGCTGCTGGAGAGTGAGCAGCCCTAGCAGGGATGGACATGATG
CTGTGTGGTGAGGGTGCTGTGTGCTCGAACCAGTGGCTGGCGCGGTGCTCCTCAGCCTGTG
TCGCTTGCTACCTCCCTGCTGCTCCCGCTGGACAGAGTGTGGACTTCCCTGGGCGCGGTGG
ACAACATGATGGTGCAGAAAGGGGACACGGCGGTGCTTAGGTGTTATTTGGAAGATGGAGCT
TCAAAGGGTGCTGGCTGAACCCGCTCAAGTATTATTTTCCGGGAGGTGATAAGTGGTCAGT
GGATCCTCGAGTTTCAATTTCAACATTGAATAAAAGGGACTACAGCCTCCAGATACAGAATG
TAGATGTGACAGATGATGGCCATACACGTGTTCTGTTTCAGACTCAACATACACCCAGAACA
ATGCAGGTGCATCTAACTGTGCAAGTTCCTCTAAGATATATGACATCTCAAATGATATGAC
CGTCAATGAAGGAACCAACGTCACCTCTTACTGTGTTGGCCACTGGGAAACAGAGCCTTCCA
TTTCTTGGCCACACATCTCCCCATCAGCAAAACCATTTGAAAAATGGACAATATTTGGACATT
TATGGAATTACAGGGACACAGGCTGGGGAATATGAATGCAGTGGGAAATGTCTGTGTCATT
CCCAGATGTGAGGAAAGTAAAGTTGTTGTCAACTTTGCTCCTACTATTAGGAAATTAAT
CTGGCACCGTGACCCCGGACGCGAGTGGCCTGATAAGATGTGAAGGTGCAGGTGTGCGCCCT
CAGCCCTTTGAATGGTACAAAGGAGAGAAAGCTCTTCAATGGCCCAACAGGAATTTAT
TCAAAATTTTACACAAGATCCATTCTCACTGTTACCAACGTGACAGGAGCACTTCGGCA
ATTATACCTGTGGCTGCGCCCAACAAGCTAGGCACAACCAATGCAGGCTGCCCTTCCACCT
CCAAGTACAGCCAGTATGGAATTACCGGAGCGCTGATGTTCTTTTCTCCTGCTGGTACCT
TGTGTTGACACTGTCCTCTTTCACAGCATATTCTACCTGAAGAATGCCATTCTACAATAAA
TTCAAAGACCCATAAAAGGCTTTTAAGGATTCTCTGAAAGCTGATGGATCCAATCT
GGTACAGTTTGTAAAAAGCAGCGTGGGATATAATCAGCAGTGCTTACATGGGGATGATCGCC
TCTGTGAGAATTGCTCATTATGTAATACTTTAATCTACTCTTTTGTGATTAGCTACATTA
CCTTGTGAAGCAGTACACATTGTCCTTTTAAAGACGTGAAAGCTCTGAAATTAATTTTAG
AGGATATTAATTTGTGATTTTCATGTTTGAATCTACAACCTTTCAAAGCATTCACTCATGGT
CTGCTAGGTTGCAGGCTGTAGTTTACAAAAACGAATATTGCAGTGAATATGTGATTTCTTAA
GGCTGCAATACAAGCATTCACTTCCTGTTTCAATAAGAGTCAATCCACATTTACAAAGATG
CAATTTTTCTTTTTTGATAAAAAAGCAAATAATATTGCCTTCAGATTATTTCTTCAAATA
TAACACATATCTAGATTTTCTGCTTGCAATGATATTCAAGTTTCAGGAATGAGCCTTGAAT
ATAACTGGCTGTGCAGCTCTGCTTCTCTTCTCTGTAAGTTCAAGTGGGTGTGCTCTCATAC
AATAATATTTTCTTTGCTCCCACTAATAAATGTTTGTCTAAATCTTCAATTTGA
AAGTAAAAATAAACAGAGTGATCAAGTTAAACCATACACTATCTCTAAGTAACGAAGGAGC
TATTTGACTGTAAAAATCTCTTCTGCACTGACAATGGGGTTTGAGAAATTTGCCCCACACT
AATCAGTTCTGTGATGAGAGACAATTTAATAACGATAGTAAATATACCAATATGATTTCT
TTTAGTTGAGCTTAAATGTTAGATCCACCGTGGGAAATCATTCCCTTTAAATGACAGCACA
GTCCACTCAAAGGATGGCTGCAATACAGCATCTTTTCTTTCACCTAGTCCAAGCCAAAA
TTTTAAGATGATTTGTGAGAAAGGCACAAAGTCTTATCACCTAATATTAAGAGTTGGTA
AGCGCTCATCATTAATTTTATTTTGTGGCAGGTATTATGACAGTCGACCTGGAGGGTATGGA
TATGGATATGGAAGTTCCAGAGACTATAATGGCAGAAACAGGGTGGTTATGACCGCTACTC
AGGAGGAAATTACAGAGACAATATGACAACCTGAAATGAGACATGCAATATATAGATACA
CAAGGAATAATTTCTGATCCAGGATCGTCTTCCAATGGCTGTATTTATAAAGGTTTGTG
AGCTGCACTGAAGCATCTTATTTTATAGTATATCAACCTTTGTTTAAATTTAAATGGCTGCCA
AGGTAGCTGAAGACCTTTTAGACAGTTCATCTTTTTTTTTAAATTTTTCTGCGCTATTTAA
AGACAATTTATGGGACGTTTGTCAAAAAAATAAAAAAAAAAAAAAAAAA

FIGURE 230

MMLLVQGACCSNQWLA AVL LLSLCCLLPSCLPAGQSVDFPWA AVDNMMVRKGD TAVLR CYLED
GASKGAWLNRSSI IFAGGDKWSVDPRVSISTLNKRDYSLQIQNV DVTDDGPYTCSVQTQHTP
RTMQVHLTVQVPPKIYDISNDMTVNEGTVTLTCLATGKPEPSISWRHISPSAKPFENGQYL
DIYGITRDQAGEYECSAENAVSFDPVRKVKV VNFAPTIQEIKSGTVTPGRSGLIRCEGAGV
PPPAFEWYKGEKKLFNGQQGII IQNFSTRSILTVTNVTQEHFGNYTCVAANKLGT TNASLPL
NPPSTAQYGITGSADVL FSCWYLVLTLS SFTSIFYLKNAILQ

Important features of the protein:

Signal peptide:

amino acids 1-31

Transmembrane domain:

amino acids 326-345

N-glycosylation sites.

amino acids 71-75, 153-157, 273-277, 284-288, 292-296, 305-309

Casein kinase II phosphorylation site.

amino acids 147-151, 208-212, 224-228

Tyrosine kinase phosphorylation site.

amino acids 178-186

N-myristoylation sites.

amino acids 7-13, 63-70, 67-73, 151-157, 239-245, 291-297,
302-308, 319-325

Myelin P0 protein:

amino acids 92-121

FIGURE 231

AGTGGTTCGATGGGAAGGATCTTTCTCCAAGTGGTTCCTCTTGAGGGGAGCATTCTGCTGG
CTCCAGGACTTTGGCCATCTATAAAGCTTGGCAATGAGAAATAAGAAAATTCTCAAGGAGGA
CGAGCTCTTGAGTGAGACCCAAACAAGCTGCTTTTCACCAAATTGCAATGGAGCCTTTTCGAAA
TCAATGTTCCAAAGCCCAAGAGGAGAAATGGGGTGAACTTCTCCCTAGCTGTGGTGGTCATC
TACCTGATCCTGCTCACCCTGGCGCTGGGCTGCTGGTGGTCCAAGTTCTGAATCTGCAGGC
GCGGCTCCGGGTCTGGAGATGTATTCTCTCAATGACACTCTGGCGGCTGAGGACAGCCCGT
CCTTCTCCTTGCTGCAGTCAGCACACCCTGGAGAACACCTGGCTCAGGGTGACATCGAGGCTG
CAAGTCTGCAGGCCCCAACTCACCTGGGTCCGCGTCAGCCATGAGCACTTGCTGCAGCGGGT
AGACAATTCACTCAGAACCCAGGGATGTTCAGAATCAAAGTGAAACAAGGCGCCCCAGGTC
TTCAAGGTCACAAGGGGCCATGGGCATGCCTGGTGCCTTGGCCCGCGGGACCCTGCT
GAGAAGGGAGCCAAGGGGGCTATGGGACGAGATGGAGCAACAGGCCCTCGGAGCCCCAAGG
CCCACCGGGAGTCAAGGGAGAGGCGGGCTTCCAAGGACCCAGGGTGCTCCAGGGAAGCAAG
GAGCCACTGGCACCCAGGACCCCAAGGAGAGAAGGCGAGCAAAGGCGATGGGGGTCTCATT
GGCCCAAAAGGGGAACTTGAACCTAAGGGAGAGAAAGGAGACCTGGGTCTCCAGGAAGCAA
AGGGGACAGGGGCATGAAAGGAGATGCAGGGGTCTATGGGGCTCTGGAGCCAGGGGAGTA
AAGGTGACTTCGGGAGGCCAGGCCACCAGGTTTGGCTGGTTCCTTGAGAGCTAAAGGAGAT
CAAGGACAACCTGGACTGCAGGGTGTTCGGGCCCTCCTGGTGCAGTGGGACACCCAGGTG
CAAGGGTGAGCCTGGCAGTGTGCTCCCTGGGCGAGCAGGACTTCCAGGGAGCCCCGGGA
GTCCAGGAGCCACAGGCTGAAAGGAAGCAAAAGGGGACACAGGACTTCAAGGACAGCAAGGA
AGAAAAGGAGAATCAGGAGTTCCAGGCCCTGCAGGTGTGAAGGGGAGAACAGGGGAGTCAAG
GCTGGCAGGTCCCAAGGGAGCCCCCTGGACAAGCTGGCCAGAAGGGAGACAGGGAGTGAAG
GATCTTCTGGGGAGCAAGGAGTAAAGGGAGAAAAAGGTGAAAGAGGTGAAAACCTCAGTGTCC
GTCAGGATTGTGCGCAGTAGTAACCGAGGCCGGGCTGAAGTTTACTACAGTGGTACCTGGGG
GACAAATTTGCGATGACGAGTGGCAAAATTCTGATGCCATTGTCTTCTGCCGATGTGGGTT
ACTCCAAAGGAAGGGCCCTGTACAAAGTGGGAGCTGGCACTGGGCAGATCTGGCTGGATAAT
GTTCAAGTGTGGGGCACGGAGAGTACCTGTGGAGCTGCACCAAGAATAGCTGGGGCCATCA
TGACTGCAGCCACGAGGAGGACGAGGCGTGGAGTGCAGCGCTGACCCCGGAAACCTTTCA
CTTCTCTGCTCCCGAGGTGTCCTCGGGCTCATATGTGGGAAGGAGAGGATCTCTGAGGAGT
TCCTTGGGACAACTGAGCAGCCTCTGGAGAGGGGCCATTAAATAAGCTCAACATCATTGA

FIGURE 232

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA68886

><subunit 1 of 1, 520 aa, 1 stop

><MW: 52658, pI: 9.16, NX(S/T): 3

MRNKKILKEDELLSETQQAAPHQIAMEPFEINVPKPKRRNGVNFSLAVVVIYLILLTAGAGL
LVVQVLNLQARLRVLEMYFLINDTLAAEDSPFSLLQSAHPGEHLAQGASRLQVLQAQLTWVR
VSHHLLQRVDNFTQNPGMFRIKGEQGAPGLQGHKGAMGMPGAPGPPGPPAEKGAKGAMGRD
GATGPGSGPQGPVGKGEAGLQGPQGAPGKQGATGTPGPQGEKGSKGDDGLIGPKGETGTGKE
KGDGLGLPGSKGDRGMKGDAGVMGPPGAQGSKGD FGRPGPPGLAGFPAGAKGDQGPGLQGVPG
PPGAVGHFPAKGEPPGSAGSPGRAGLPGSPGSPGATGLKGSKGD TGLQCGQGRKGESGVPGPA
GVKGEQGSPLAGPFGAPGQAGQKGDQGVKGSSEBQGVKGEKGERGENSVSVRIVGSSNRGR
AEVYYSGTWGTICDDEWQNSDAIVFCRMLGYSKGRALYKVGAGTGQIWLNDNVQCRGTESTLW
SCTKNSWGHHDCSHEEDAGVECSV

Transmembrane domain:

amino acids 47-66 (type II)

N-glycosylation sites.

amino acids 43-47, 83-87, 136-140

Tyrosine kinase phosphorylation site.

amino acids 432-440

N-myristoylation sites.

amino acids 41-47, 178-184, 253-259, 274-280, 340-346, 346-352,
400-406, 441-447, 475-481, 490-496, 515-521

Amidation site.

amino acids 360-364

Leucine zipper pattern.

amino acids 56-78

Speract receptor repeat

amino acids 422-471, 488-519

Clq domain proteins.

amino acids 151-184, 301-334, 316-349

FIGURE 233

CCCACGCGTCCGAAGGCAGACAAAGGTTCAATTTGTAAAGAAGCTCCTTCCAGCACCTCCTCT
CTTCTCCTTTTGCCCAAACCTACCCAGTGAGTGTGAGCATTTAAGAAGCATCCTCTGCCAAG
ACCAAAAGGAAAGAAGAAAAAGGGCCAAAAGCCAAAATGAAACTGATGGTACTTGTTTTCAC
CATTGGGCTAACTTTGCTGCTAGGAGTTCAAGCCATGCCTGCAAATCGCCTCTCTTGCTACA
GAAAGATACTAAAAGATCACAACTGTCACAACCTTCGGAAGGAGTAGCTGACCTGACACAG
ATTGATGTCAATGTCCAGGATCATTTCTGGGATGGGAAGGGATGTGAGATGATCTGTTACTG
CAACTTCAGCGAATTGCTCTGCTGCCCAAAAGACGTTTTCTTTGGACCAAAGATCTCTTTCG
TGATTCCTTGCAACAATCAATGAGAATCTTCATGTATTCTGGAGAACACCATTCCTGATTTC
CCACAACTGCACTACATCAGTATAACTGCATTTCCTAGTTTCTATATAGTGCAATAGAGCAT
AGATTCTATAAATCTTACTTGTCTAAGACAAGTAAATCTGTGTTAAACAAGTAGTAATAAA
AGTTAATTCAATCTAAAAAAAAAAAAA

1000
900
800
700
600
500
400
300
200
100
0

FIGURE 234

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52758

<subunit 1 of 1, 98 aa, 1 stop

<MW: 11081, pI: 6.68, NX(S/T): 1

MKLMVLVFTIGLTLLLGVDQAMPANRLSCYRKILKDHCHNLPEGVADLTQIDVNVQDHFWDG
KGCEMICYCNFSELLCCPKDVFFGPKISFVIPCNNQ

Important features:

Signal peptide:

amino acids 1-20

N-glycosylation site.

amino acids 72-76

Tyrosine kinase phosphorylation site.

amino acids 63-71

FIGURE 235

CCCACGCGTCCGCGGACGCGTGGGCTGGACCCAGGCTCTGGAGCGAATTCCAGCCTGCAGGG
CTGATAAGCGAGGCATTAGTGAGATTGAGAGAGACTTTACCCGCGCGTGGTGGTTGGAGGGC
GCGCAGTAGAGCAGCAGCACAGGCGCGGGTCCCGGGAGGCCGGCTCTGCTCGCGCCGAGATG
TGGAATCTCCTTCACGAAACCGACTCGGCTGTGGCCACCGCGCGCCGCCGCTGGCTGTG
CGCTGGGGCGCTGGTGTGGCGGGTGGCTTCTTTCTCCTCGGCTTCCTCTTCGGGTGGTTTA
TAAATCCTCCAATGAAGCTACTAACATTACTCCAAAGCATAATATGAAAGCATTCTTGGAT
GAATTGAAAGCTGAGAACATCAAGAAGTTCTTACATAATTTTACACAGATACCACATTTAGC
AGGAACAGAACAAATCTTACAGCTTGCAAAGCAAATTCATCCAGTGGAAAGAATTTGGCC
TGGATTCTGTTGAGCTAGCTCATTATGATGTCTGTGTCTCTACCCAAATAAGACTCATCCC
AACTACATCTCAATAATTAATGAAGATGGAAATGAGATTTTCAACACATCATTATTGAAACC
ACCTCCTCCAGGATATGAAATGTTTCGGATATGTACCACCTTTTCAGTGCTTTCTCTCCTC
AAGGAATGCGCAGAGGGCGATCTAGTGTATGTTAACTATGCACGAACTGAAGACTTCTTTAA
TTGGAACGGGACATGAAATCAATTGCTCTGGGAAAAATTGTAATTGCCAGATATGGGAAAGT
TTTCAGAGGAAATAAGGTTAAAAATGCCAGCTGGCAGGGGGCCAAAGGAGTCATTCTCTACT
CCGACCTCTGTGACTACTTTTGTCTCTGGGGTGAAGTCTTATCCAGCAGGTGGGAATCTCTC
GGAGGTGGTGTCCAGCGTGGAATATCTCTAAATCTGAATGGTGCAGGAGACCTCTCACACC
AGGTTACCCAGCAAAATGAATATGCTTATAGGCGTGAATTCAGAGGCTGTTGGTCTTCCAA
GTATTCCTGTTTCATCCAATTGGATACTATGATGCACAGAAGCTCTAGAAAAAATGGGTGGC
TCAGACCAACAGATAGCAGCTGGAGAGGAAGTCTCAAAGTGCCCTACAATGTTGGACCTGG
CTTTACTGGAACCTTTTCTACAAAAAGTCAAGATGCACATCACTCTACAATGAAGTGA
CGAGAATTACAATGTATAGGTACTCTCAGAGGAGCAGTGAACCAGACAGATATGTCATT
CTGGGAGGTCACCGGGACTCATGGGTGTTTGGTGGTATTGACCTCAGAGTGGAGCAGCTGT
TGTTTCATGAAATTGTGAGGAGCTTGGAACTGAAAAAGGAAGGGTGGAGACCTAGAAGAA
CAATTTTGTGCAAGCTGGGATGCAGAGAATTGGTCTTCTTGGTTCTACTGAGTGGGCA
GAGGAGAATTCAGACTCTTCAAGAGCGTGGCGTGGCTTATATTAATGCTGACTCATCTAT
AGAAGGAAACTACACTCTGAGAGTTGATTGTACACCGCTGATGTACAGCTTGGTACAAACC
TAACAAAAGAGCTGAAAAGCCCTGATGAAGGCTTTGAAGGCAATCTCTTTATGAAAGTTGG
ACTAAAAAAGTCCCTCCCAAGATTTCAGTGGCATGCCAGGATAAGCAAAATTTGGGATCTGG
AAATGATTTTGAGGTGTTCTTCCAACGACTTGAATGCTTCAGGCAGAGCACGGTATACTA
AAAAATTGGGAAACAAACAATTTCAGCGGCTATCCACTGTATCACAGTGTCTATGAAACATAT
GAGTTGGTGGAAAAGTTTATGATCCAATGTTTAAATATCACCTCAGTGTGGCCAGGTTTCG
AGGAGGGATGGTGTGTTGAGCTAGCCAATTCATAGTGCTCCCTTTTGATTGTGAGATTATG
CTGTAGTTTAAAGAAAGTATGCTGACAAAAATCTACAGTATTTCTATGAAACATCCACAGGAA
ATGAAGACATACAGTGTATCATTGTATTCACTTTTCTGCAAGTAAAGAAATTTTACAGAAAT
TGCTTCCAAGTTCAGTGAGAGACTCCAGGACTTTGACAAAAGCAACCAATAGTATTAGAA
TGATGAATGATCAACTCATGTTTCTGGAAGAGCATTTATTGATCATTAGGCTTACAGAC
AGGCTCTTTTATAGGCATGTCATCTATGCTCCAAGCAGCCACAACAAGTATGCAGGGGAGTC
ATTCCAGGAATTTATGATGCTCTGTTTGATATTGAAAGCAAAGTGGACCTTCCAAGGCCCT
GGGGAGAAGTGAAGAGACAGATTATGTTGAGCCCTTACAGTCAGGCGAGCTGCAGAGACT
TTGAGTGAAGTAGCCTAAGAGGATTTTATAGAGAATCCGATATTGAATTTGTGTGGTATGTCA
CTCAGAAAGAAATCGTATGGGTATATTGATAAATTTTAAATTTGGTATATTGAAATAAAGT
TGAATATTATATATA

FIGURE 236

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA52756

><subunit 1 of 1, 750 aa, 1 stop

><MW: 84305, pI: 6.93, NX(S/T): 10

MWLLHETDSAVATARRPRWLCAGALVLAGGFLLGFLFGWFIKSSNEATNITPKHNMKAFLL
DELKAENIKKFLHNFTQIPHLAGTEQNFQLAKQIQSQWKEFGLDSVELAHYDVLLSYPNKTH
PNYISIINEDGNEIFNTSLFEPPPPGYENVSDIVPPPSAFSPQGMPEGDLVYVNYARTEDFF
KLERDMKINCSGKIVARYGKVFGRGNKVKNQLAGAKGVILYSDPADYFAPGVKSYPDGWNLL
PGGGVQRGNILNLNGAGDPLTPGYPANEYAYRRGIAEAVGLPSIPVHPIGYYDAQKLEKMG
GSAPPDSSWRGSLKVPYNVGPFGFTGNFSTQKVKMHIHSTNEVTRIYNVIGTLRGAVEPDRYV
ILGGHRDSWVFGIDPQSGAAVVEIVRSFGTLKKEGWRPRRTILFASWDABEFGLLGSTEW
AEENSRLQERGVAYINADSSIEGNYTLRVDCITPLMYSLVHNLTKEKSPDEGFEGKSLYES
WTKKSPSPFESGMPRIKSLGSGNDFEVFFQRLGIASGRARYTKNWTENKFSGYPLYHVSUYET
YELVEKFYDPMFKYHLTVAQVRGGMVFELANSIVLPFDRCRDYAVVLRKYADKIYSISMKHPQ
EMKTYSVSFDLSLSAVKNFTEIASKFSERLQDFDKSNPIVLRMMNDQMLFLERAFIDPLGLP
DRPFYRHVIYAPSSHNKYAGESFPGIYDALFDIESKVDPSKAWGEVKRQIYVAAFTVQAAA
TLSEVA

Signal sequence:

amino acids 1-40

N-glycosylation sites.

amino acids 76-80, 121-125, 140-144, 153-157, 195-199, 336-340,
459-463, 476-480, 638-642

Tyrosine kinase phosphorylation sites.

amino acids 363-372, 605-613, 606-613, 617-626

N-myristoylation sites.

amino acids 85-91, 168-174, 252-258, 256-262, 282-288, 335-341,
360-366, 427-433, 529-535, 707-713